

Fig. 1A

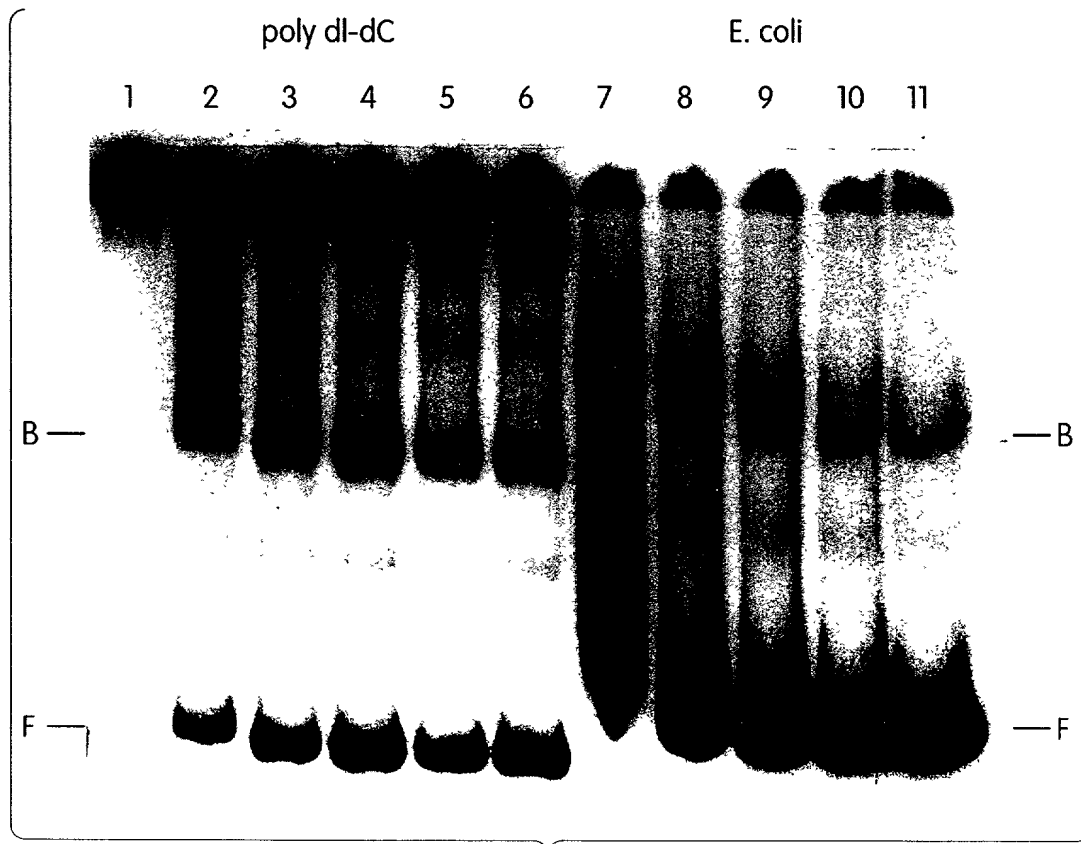


Fig. 1B

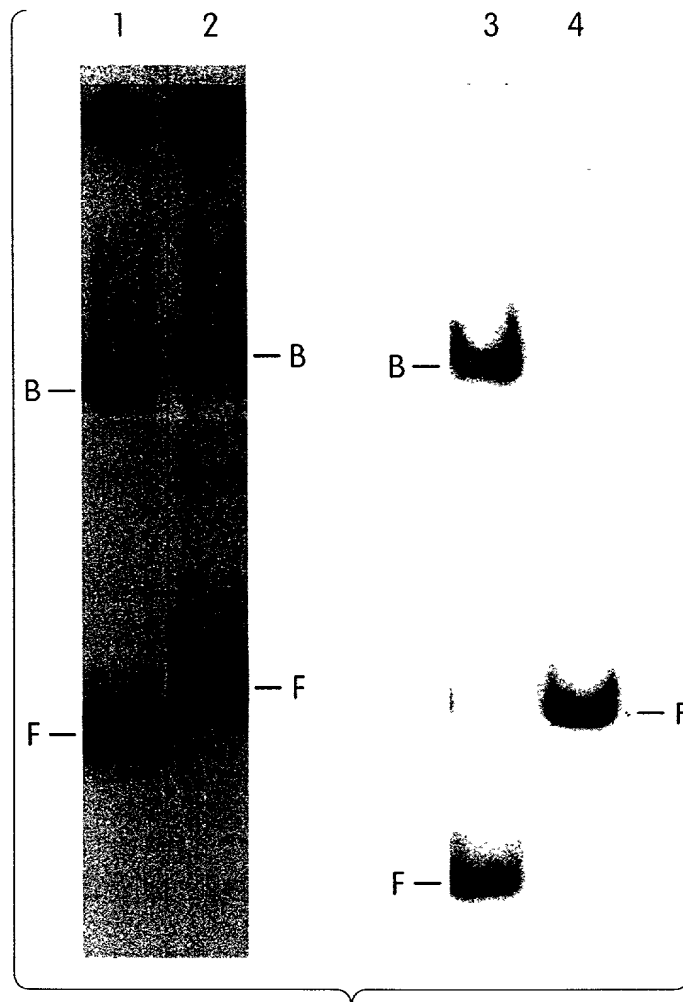


Fig. 1C

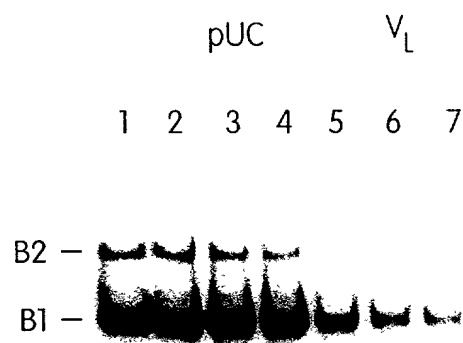
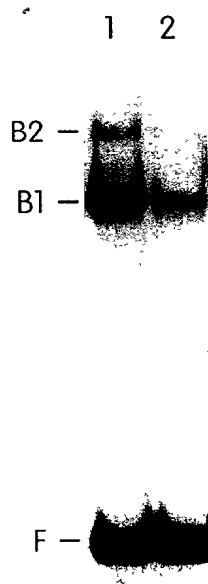


Fig. 2A



HeLa

Fig. 2B



Fig. 3

	*		*
V <sub>L</sub> coding strand (-66)	TCTTAATA	ATTTGCAT	ACCCTCAC
V <sub>H</sub> non-coding strand (-50)	CGCACATG	ATTTGCAT	ACTCATGA
J <sub>H</sub> - C <sub>μ</sub> coding strand (166)	CCTGGGTA	ATTTGCAT	TTCTAAAA

Fig. 4A

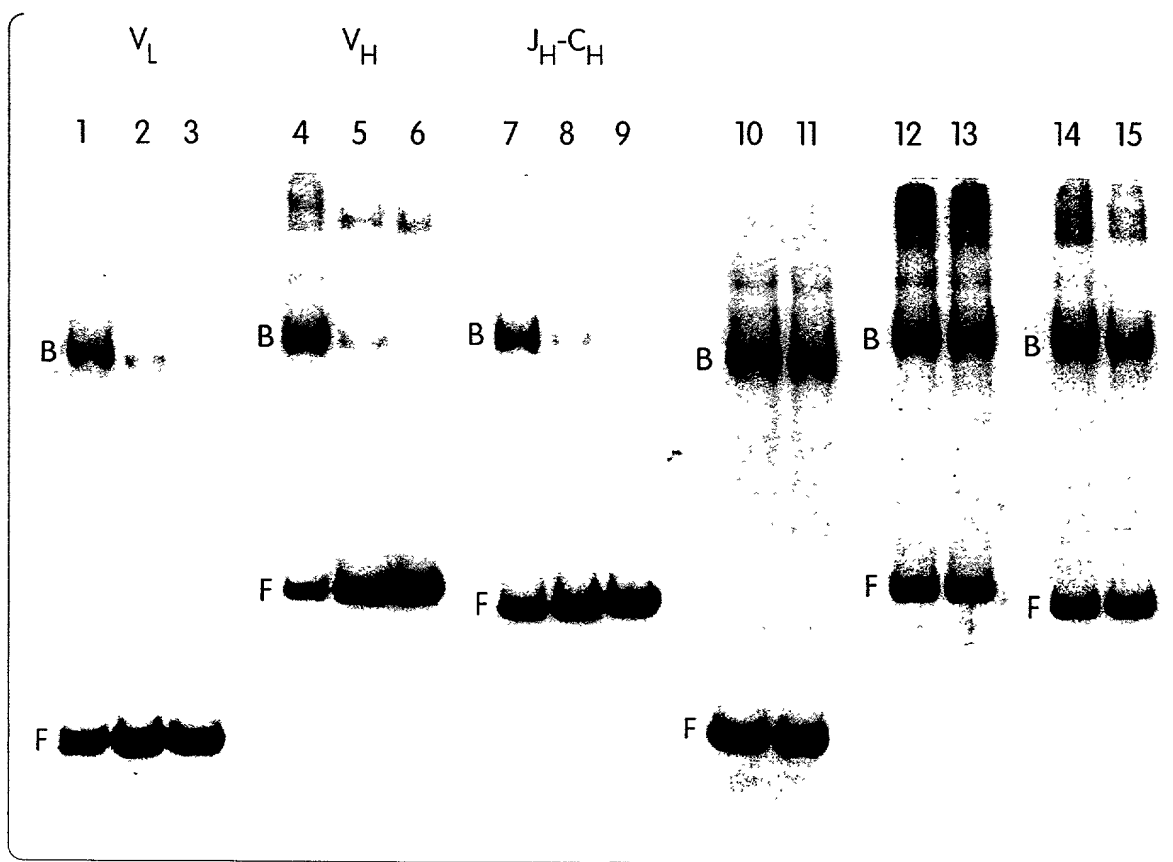


Fig. 4B

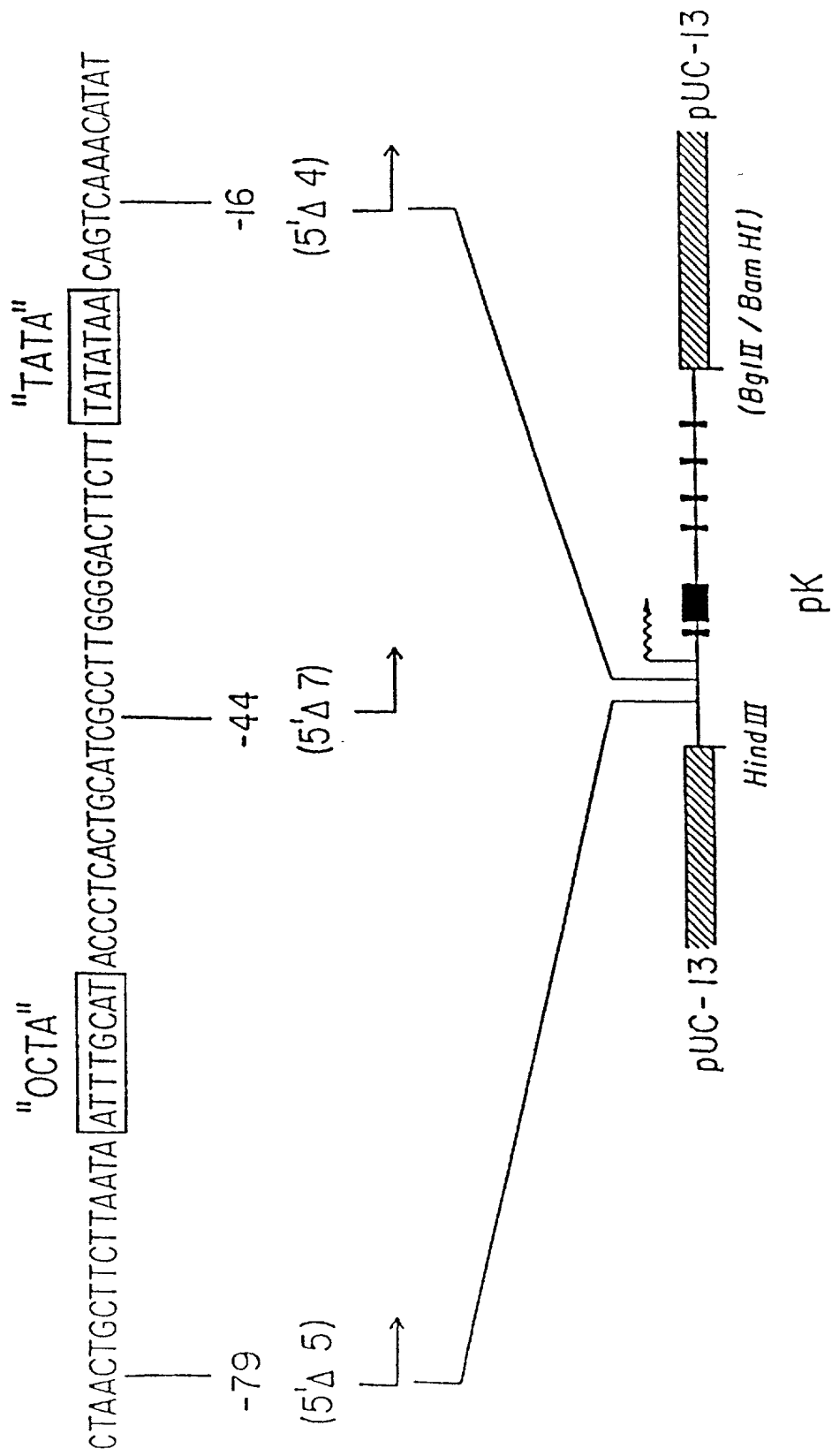


Fig. 5A

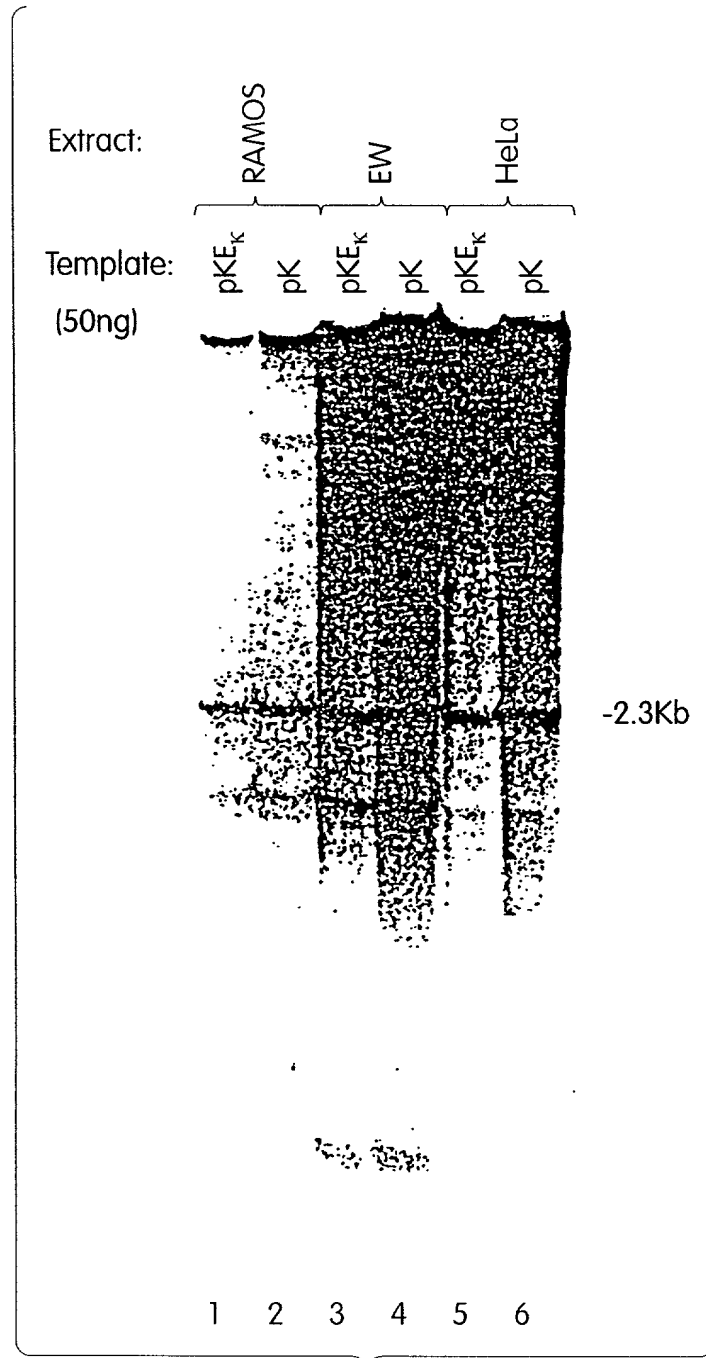


Fig. 5B

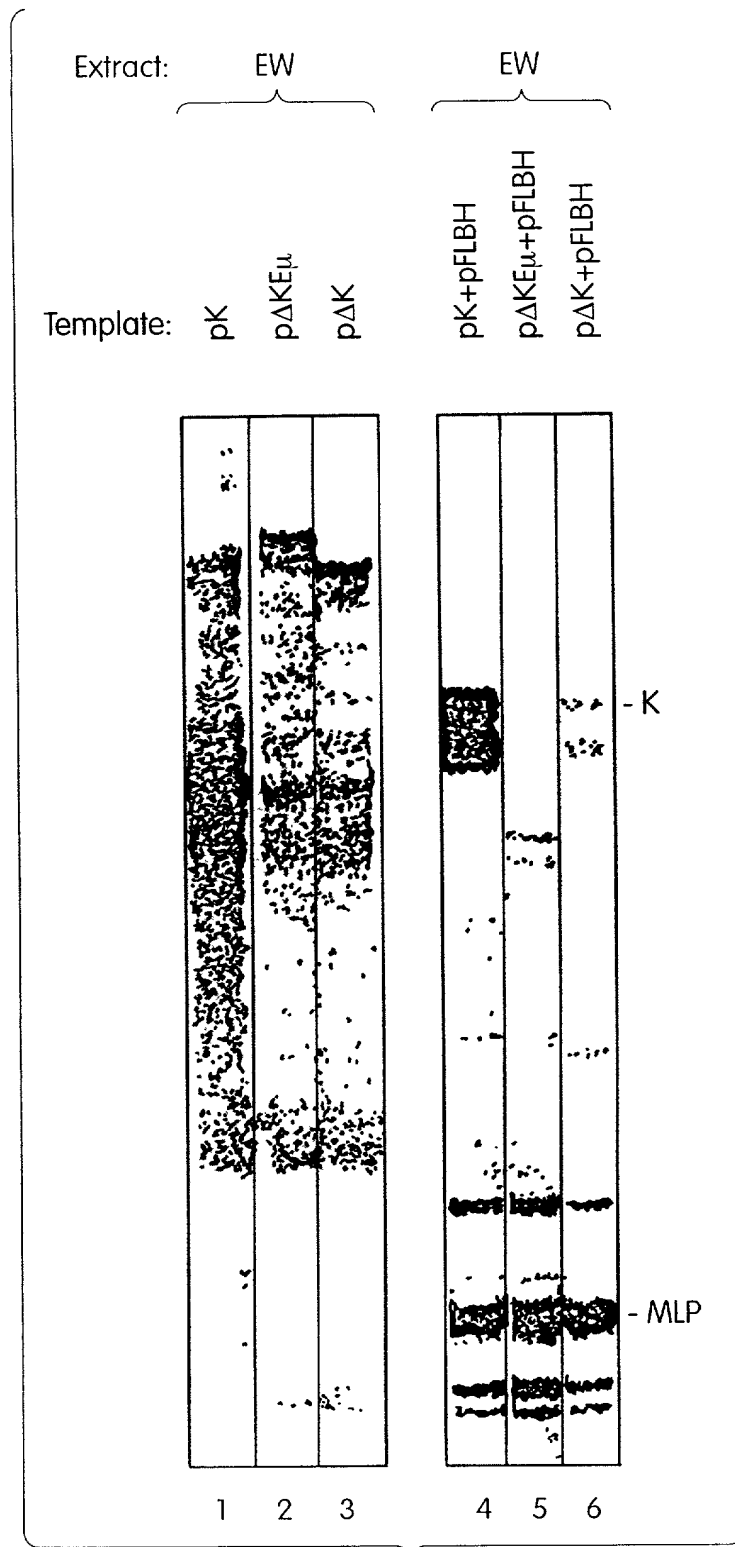


Fig. 6



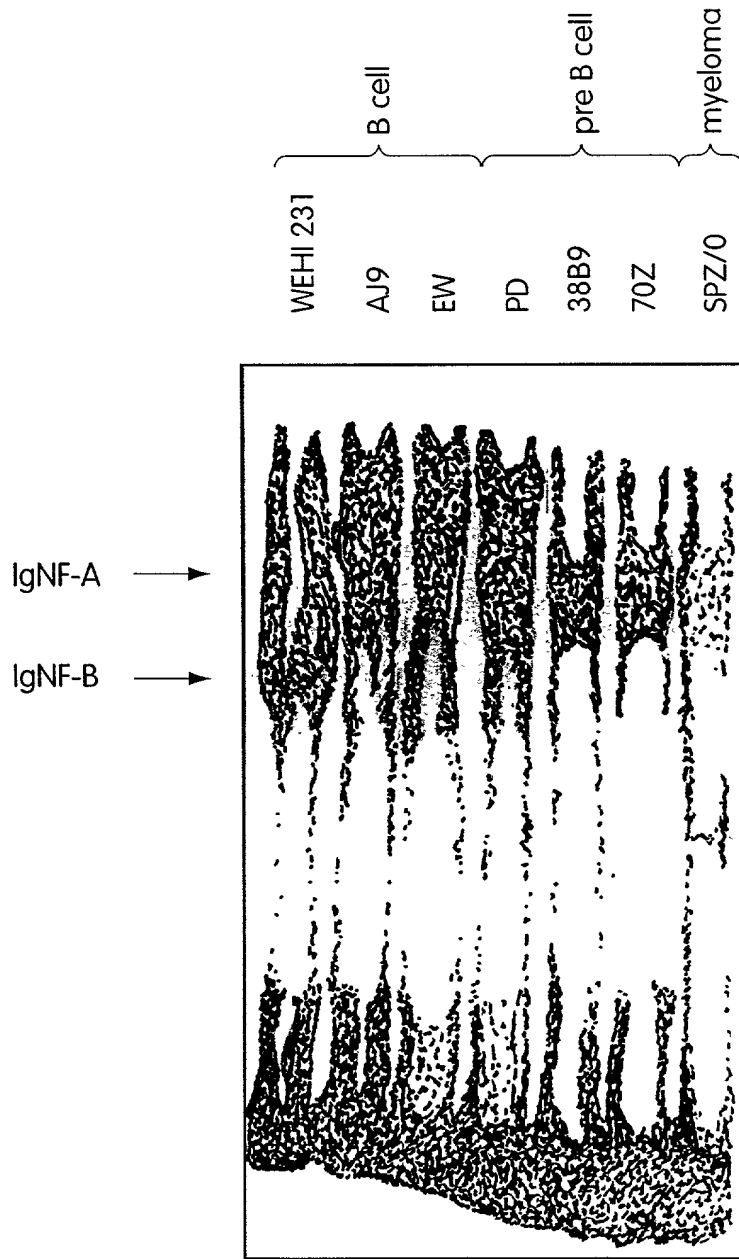


Fig. 7

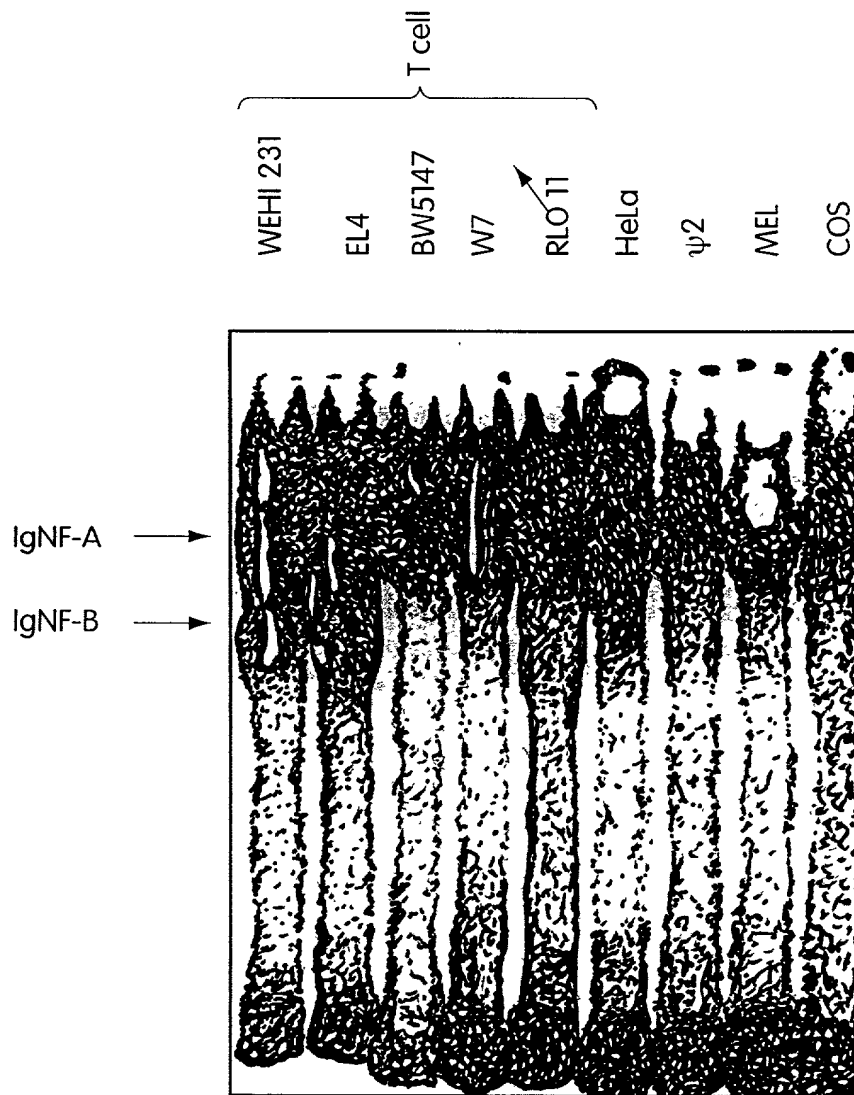


Fig. 8

Figure 9A

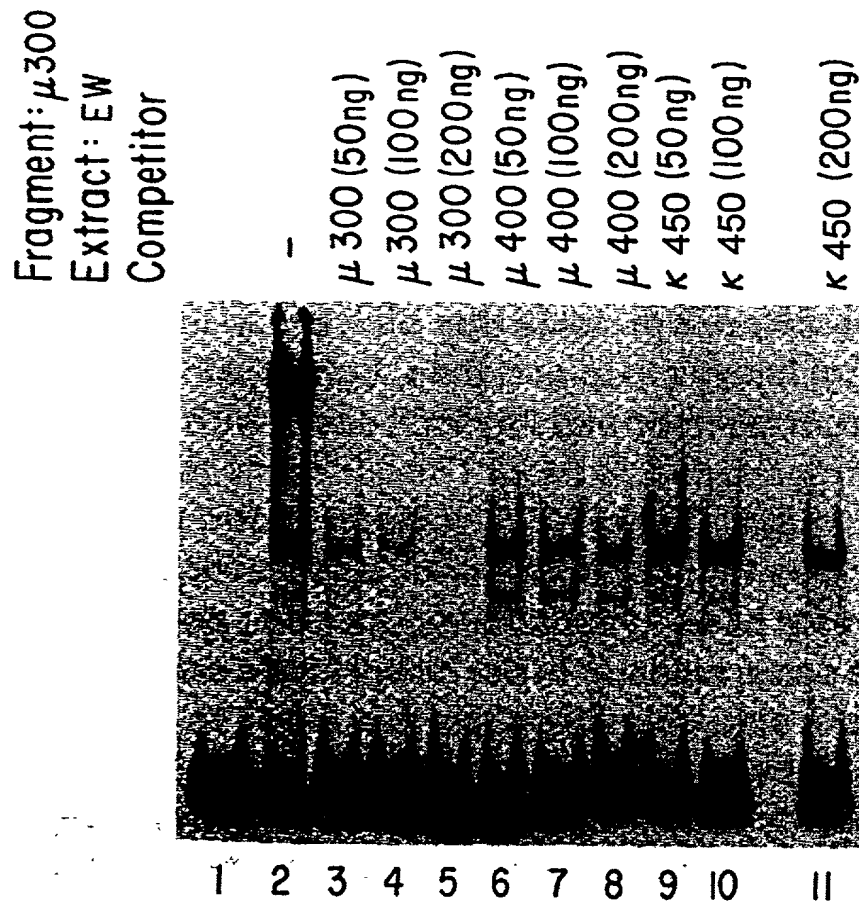
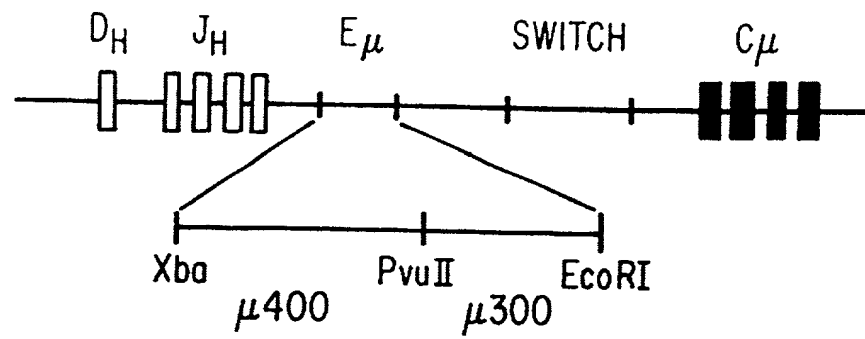


Figure 9B

Figure 10A

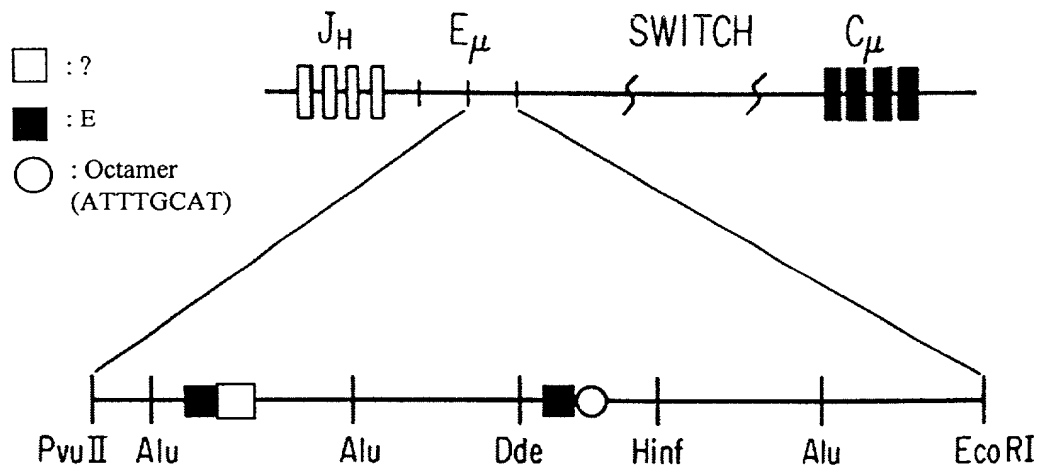
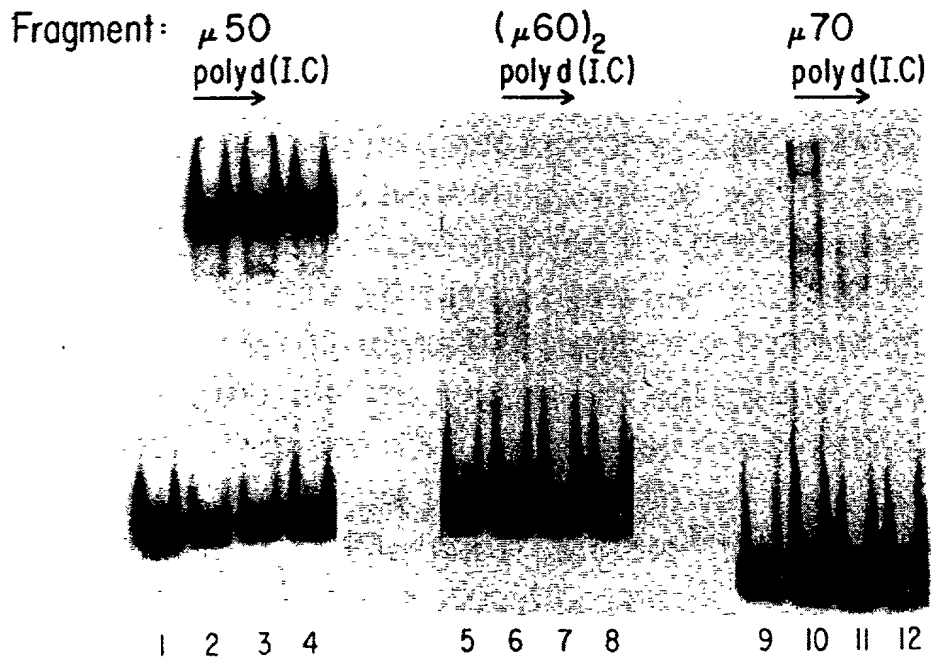


Figure 10B



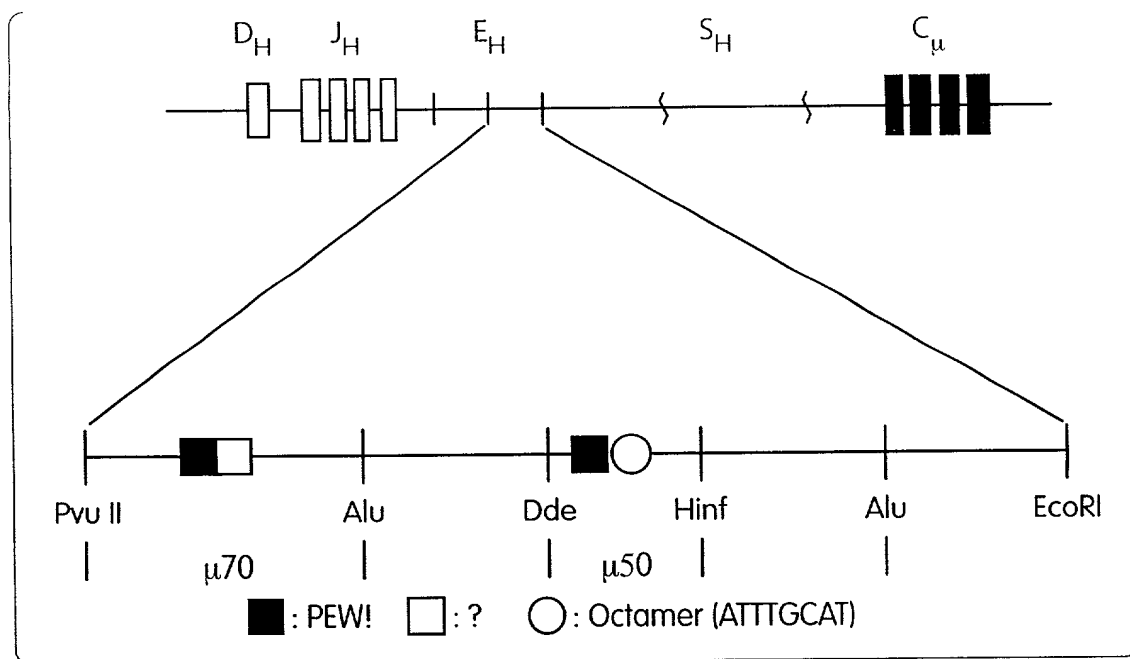


Fig. 10C

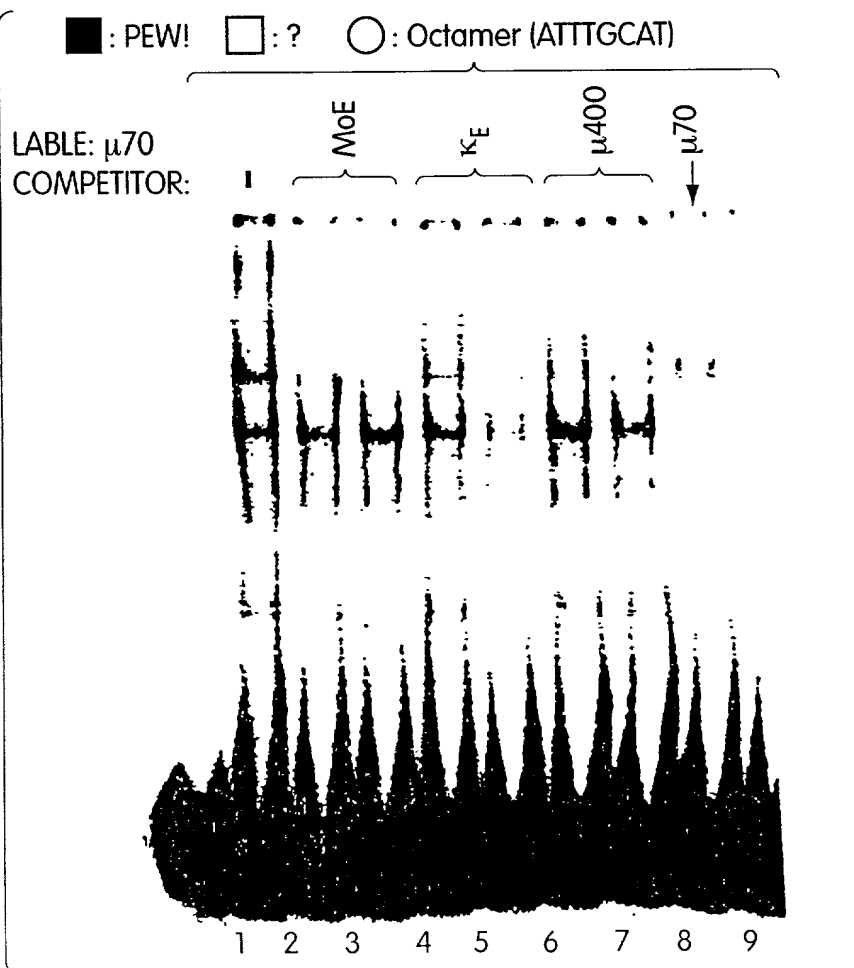


Fig. 10D

Figure 10E

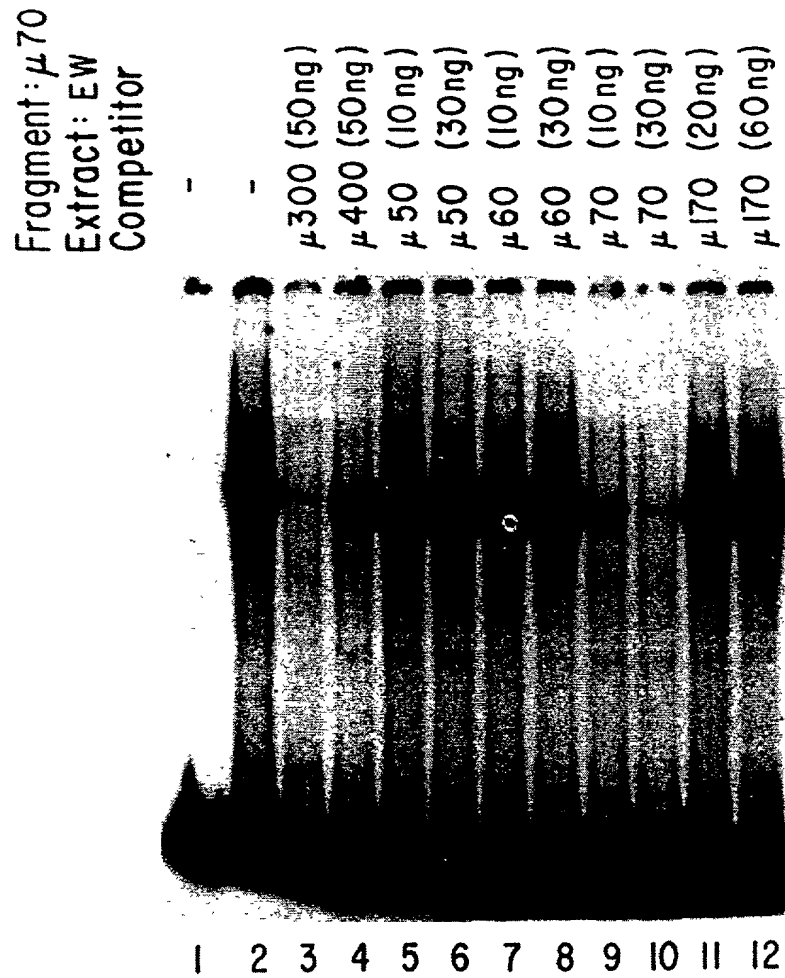
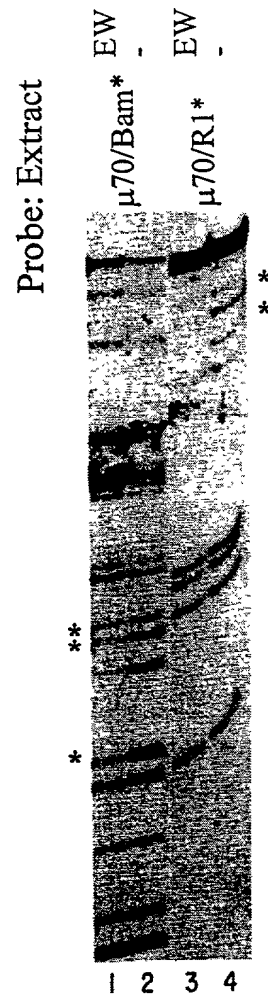


Figure 11A



Figure 11B



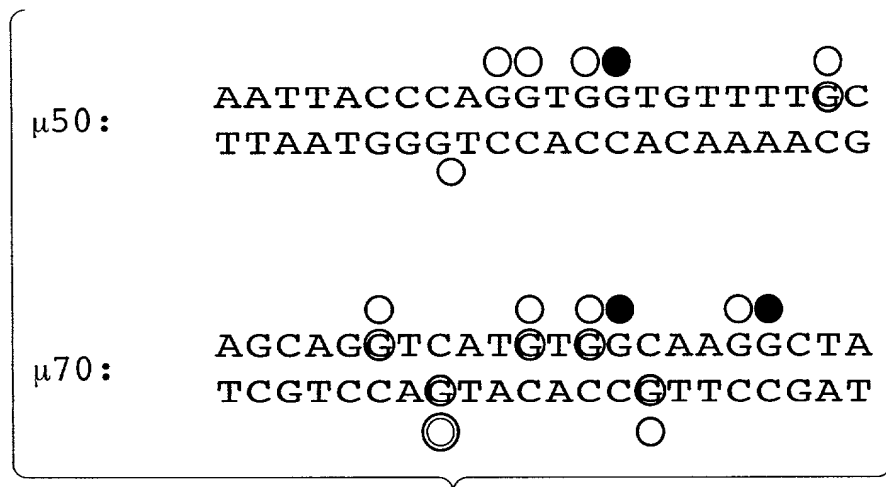


Fig. 11C



Figure 12A

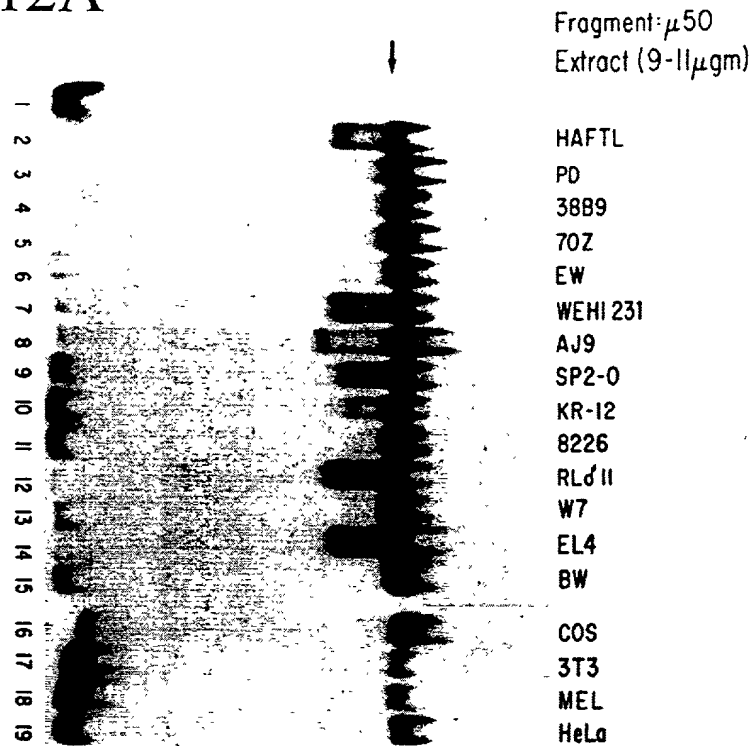


Figure 12B

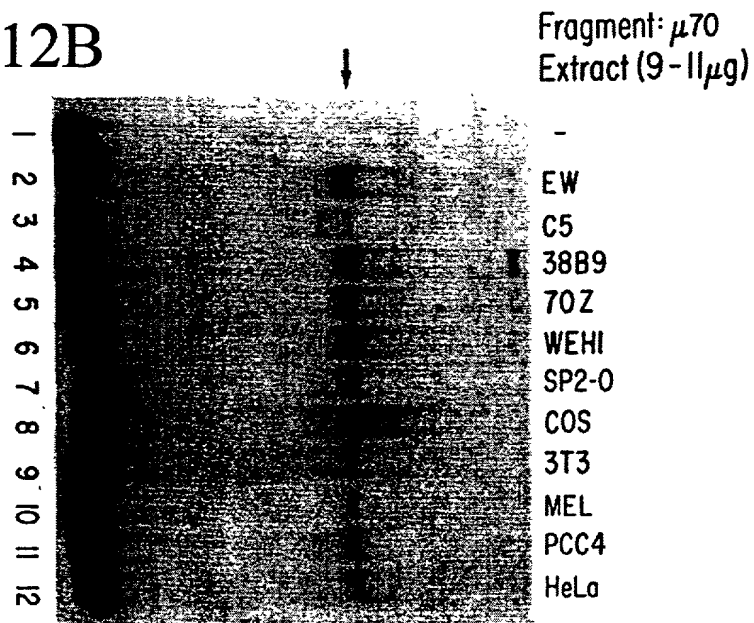


Figure 13A

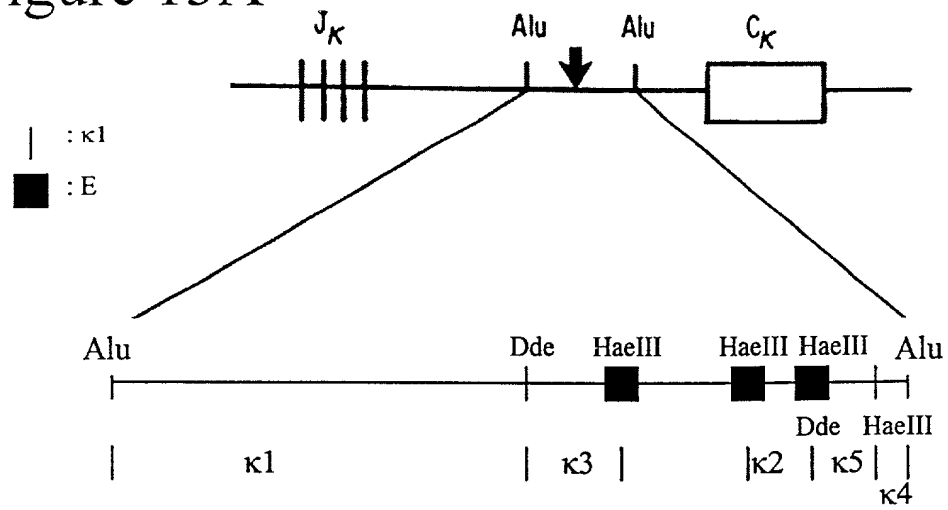


Figure 13B

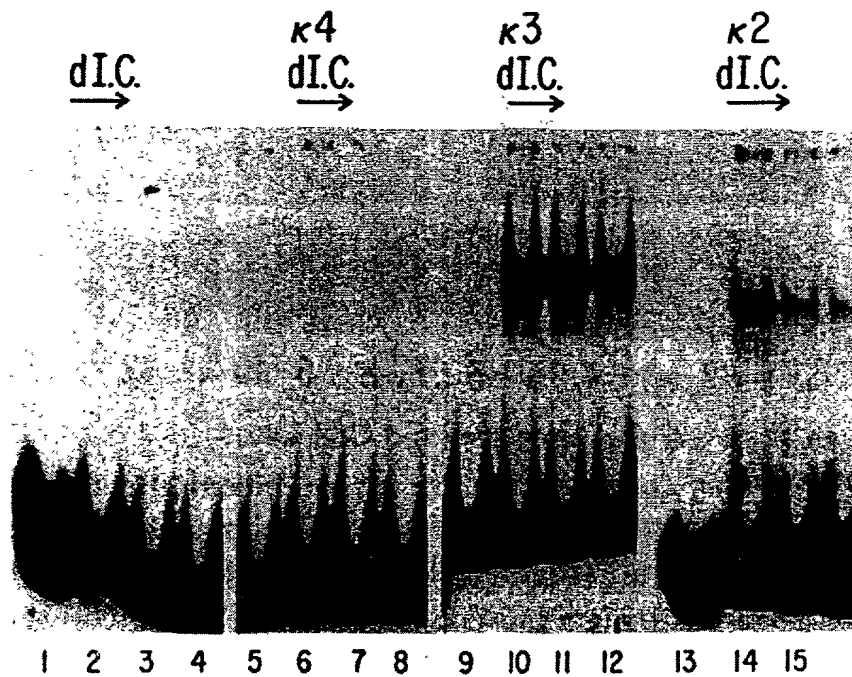


Figure 13C

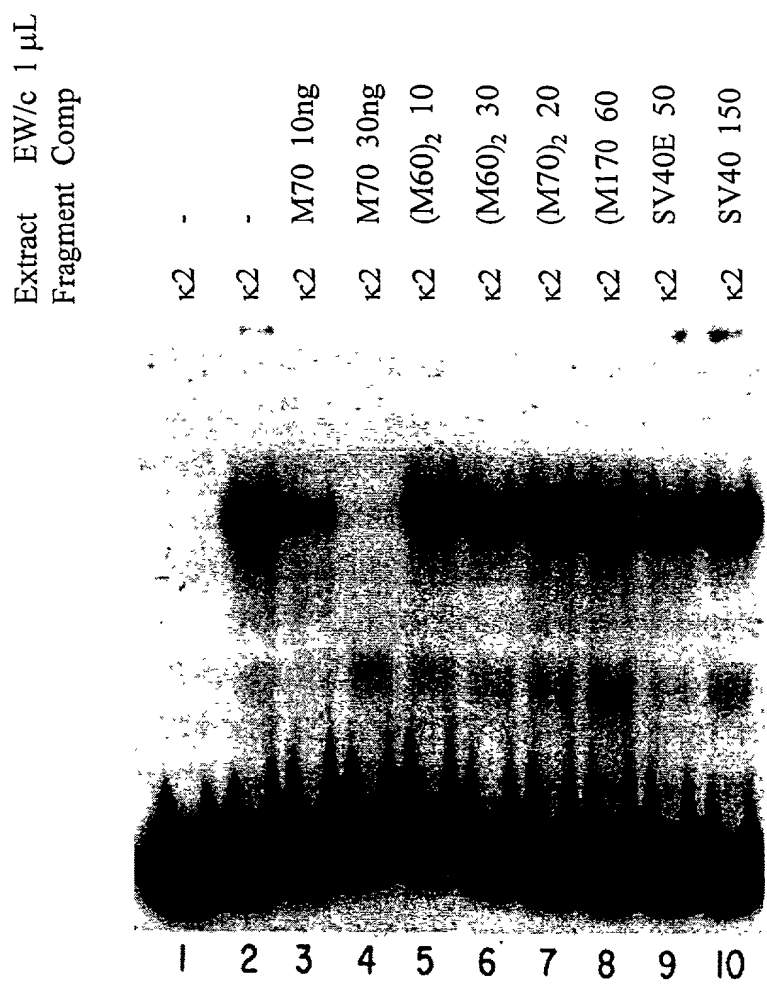
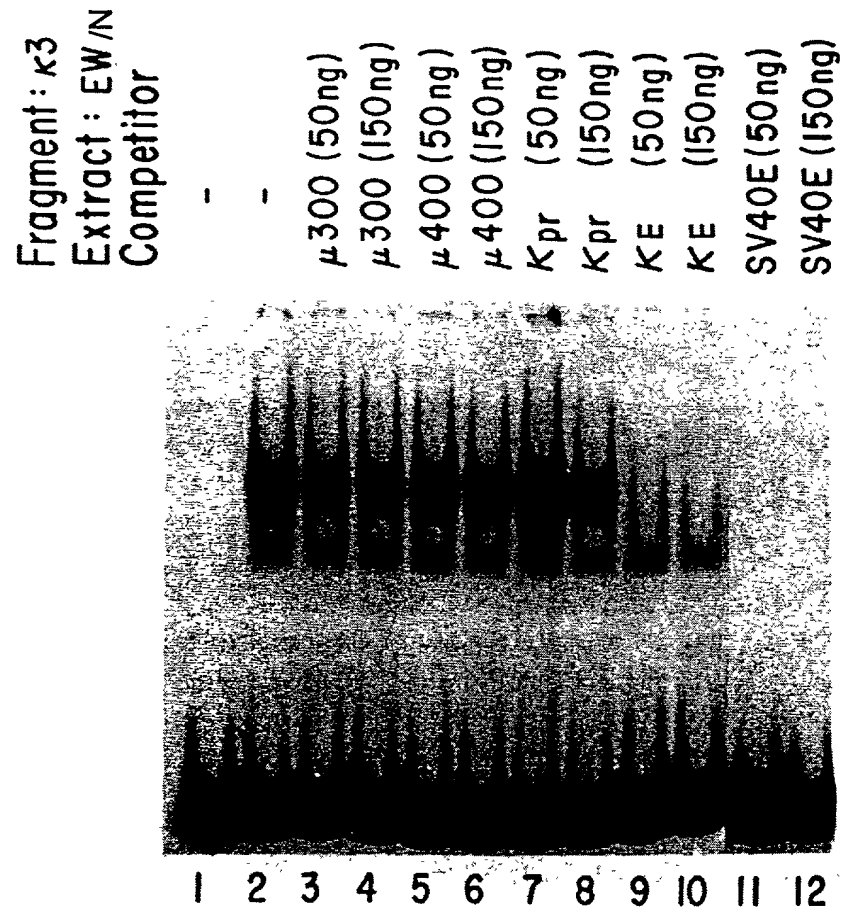


Figure 13D



Fragment:  $\kappa$ -3 /Dde\*

Extract

MPCII  
-  
WEHI 231  
-

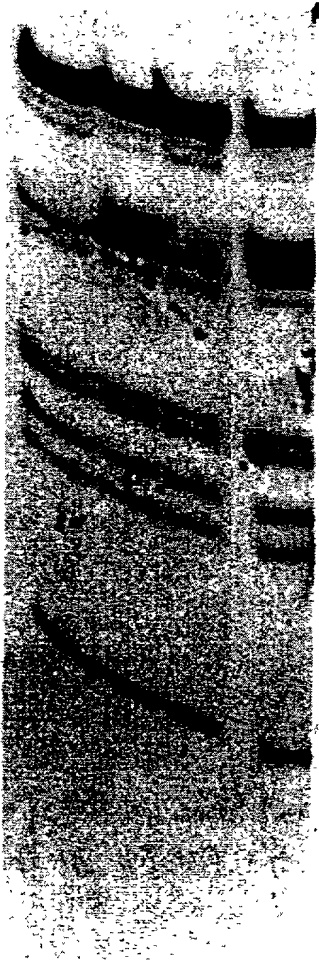


Figure 14

Figure 15A

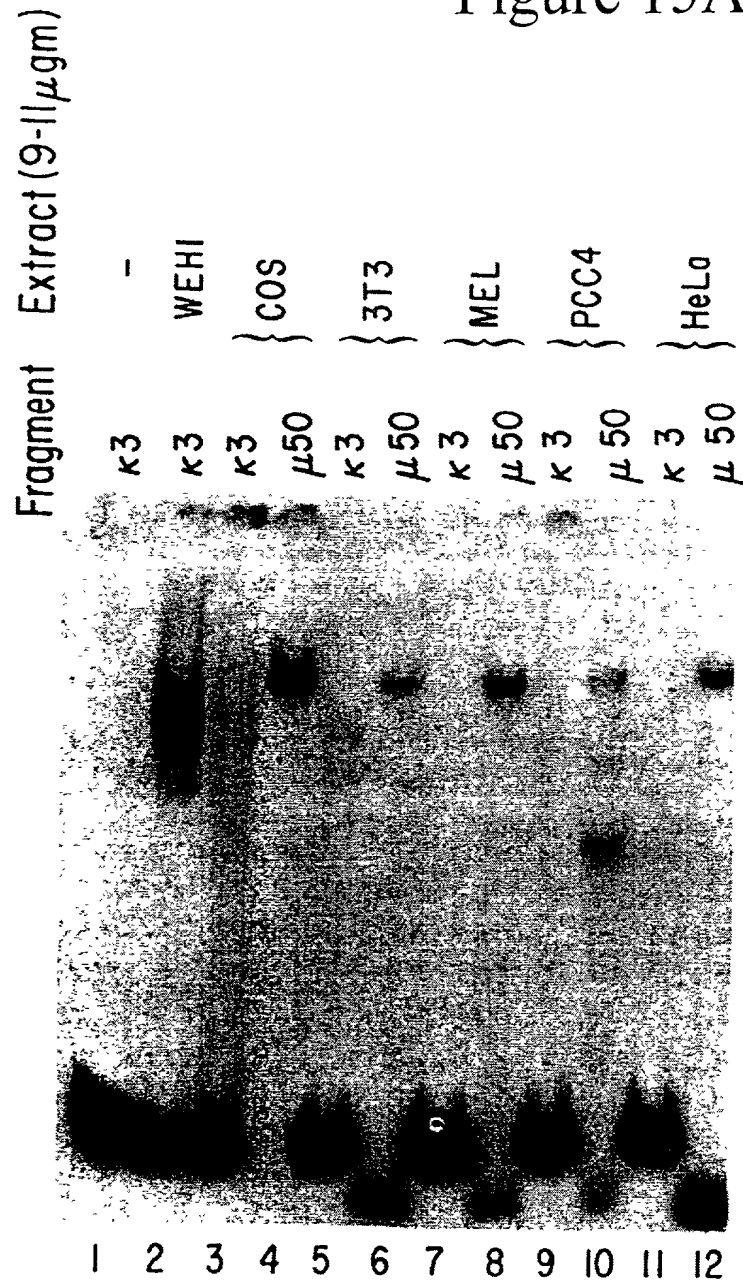
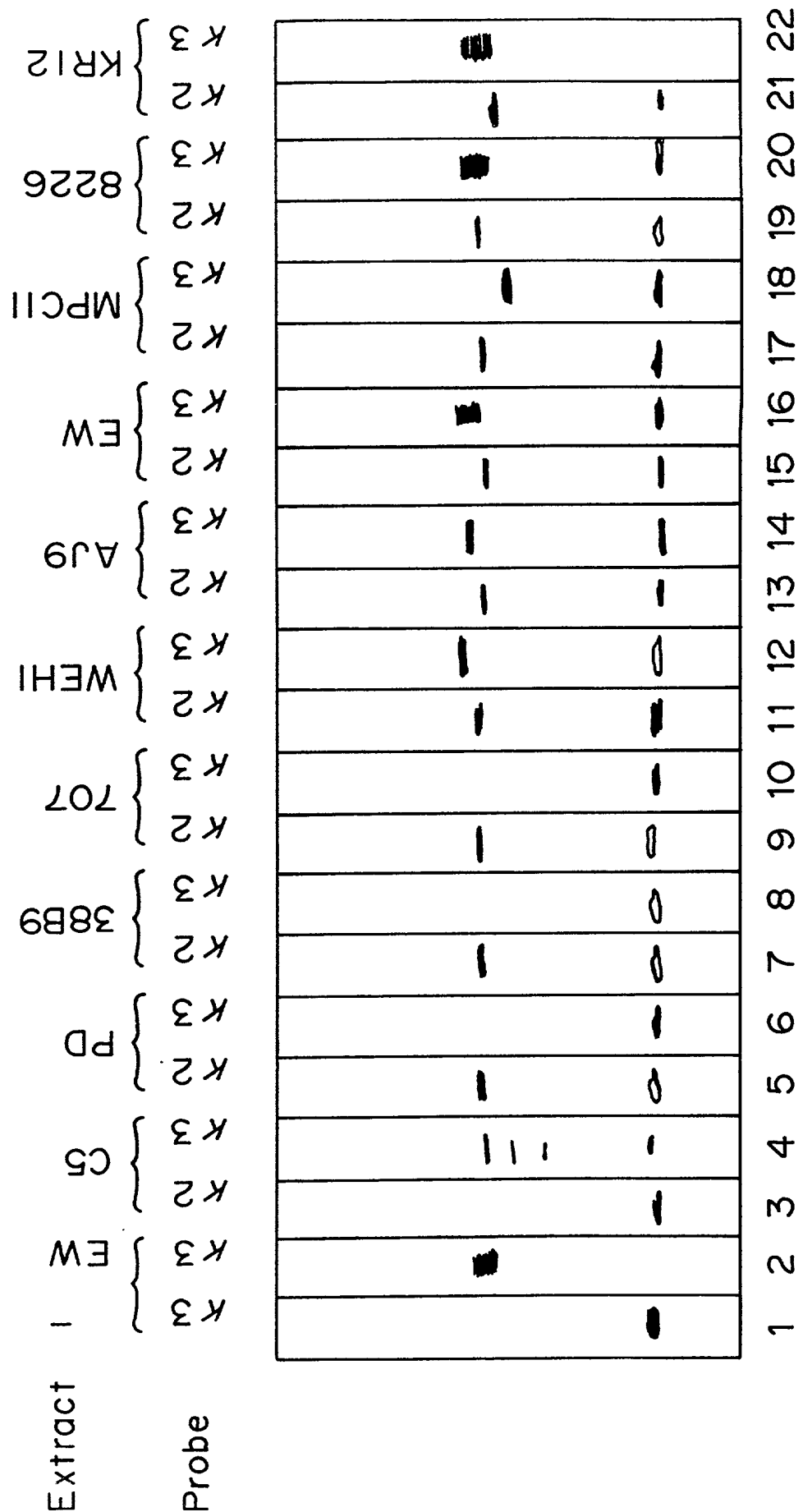


FIGURE 15b



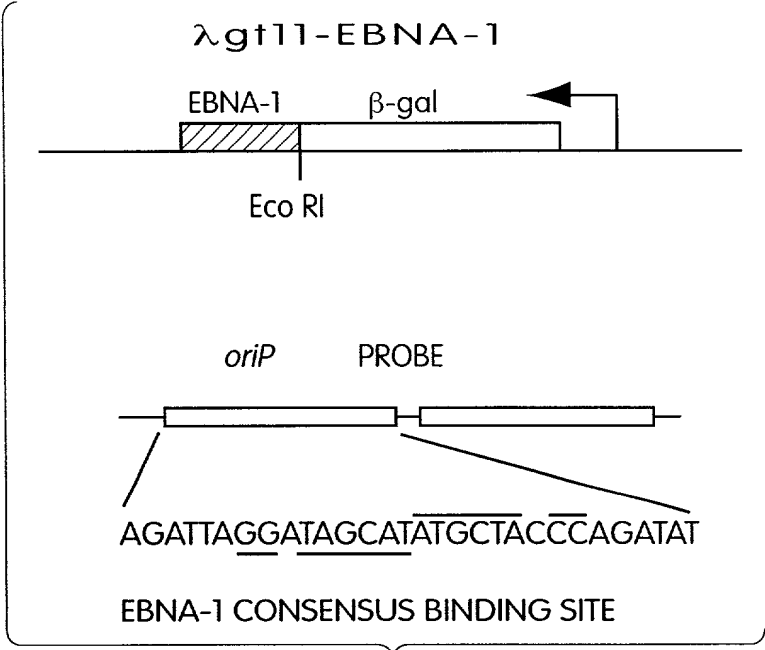


Fig. 16

MHC	<u>TGGGGATTCCCCA</u>
mhc1	TGcGGATTCCCaA
$\kappa$ EN	aGGGGACTttCCg
$\kappa$ en	aaattAcTttCCg
	a
SVEN	TGGGGAcTttCCA
HIV	TGGGGAcTttCCA
	aaGGGAcTttCCg

Fig. 17



CTGGGGCCCCCAGAGAGGGTGGGGAGATGACACAGTTGTTCCCCCAGCCCTGGCGGGGGCG  
 1 -----+-----+-----+-----+-----+-----+-----+

GGCAGCATGGTTCACTCCAGCATGGGGGCTCCAGAAATAAGAATGTCTAAGCCCCTGGAG  
 61 -----+-----+-----+-----+-----+-----+-----+  
 M V H S S M G A P E I R M S K P L E

GCCGAGAAGCAAGGTCTGGACTCCCCATCAGAGCACACAGACACCGAAAGAAATGGACCA  
 121 -----+-----+-----+-----+-----+-----+-----+  
 A E K Q G L D S P S E M T D T E R N G P

GACACTAATCATCAGAACCCCCAAAATAAGACCTCCCCATTCTCCGTGTCCCCAACTGGC  
 181 -----+-----+-----+-----+-----+-----+-----+  
 D T N H O N P Q N R T S P F S V S P T G

CCCAGTACAAAGATCAAGGCTGAAGACCCCAGTGGCGATTTCAGCCCCAGCAGCACCCCTG  
 241 -----+-----+-----+-----+-----+-----+-----+  
 P S T K I K A E D P S G D S A P A A P L

CCCCCTCAGCCGGCCCAGCCTCATCTGCCCCAGGCCCAACTCATGTTGACGGGCAGCCAG  
 301 -----+-----+-----+-----+-----+-----+-----+  
 P P Q P A Q P N L P Q A Q L M L T G S Q

CTAGCTGGGGACATACAGCAGCTCCTCCAGCTCCAGCAGCTGGTGCTTGCGCCAGGCCAC  
 361 -----+-----+-----+-----+-----+-----+-----+  
 L A G D I Q Q L L Q L Q Q L V L V P G H

CACCTCCAGCCACCTGCTCAGTTCCTGCTACCGCAGGCCCAGCAGAGCCAGCCAGGCCTG  
 421 -----+-----+-----+-----+-----+-----+-----+  
 H L Q P P A Q F L L P Q A Q Q S Q P G L

CTACCGACACCAAATCTATTCCAGCTACCTCAGCAAACCCAGGGAGCTCTTCTGACCTCC  
 481 -----+-----+-----+-----+-----+-----+-----+  
 L P T P H L F Q L P Q Q T Q G A L L T S

CAGCCCCGGGGCCGGGCTTCCCACACAGGCCGTGACCCGCCCTACGCTGCCCGACCCGCAC  
 541 -----+-----+-----+-----+-----+-----+-----+  
 Q P R A G L P T Q A V T R P T L P D P H

CTCTCGCACCCGCAGCCCCCAAATGCTTGGAGCCACCATCCCACCCCGAGGAGCCCAGT  
 601 -----+-----+-----+-----+-----+-----+-----+  
 L S H P Q P P K C L E P P S H P E E P S

GATCTGGAGGAGCTGGAGCAATTGGCCCCGACCTTCAAGCAACGCCGCATCAAGCTGGGC  
 661 -----+-----+-----+-----+-----+-----+-----+  
 D L E E L E Q F A R T F K Q R R I K L G

TTCACGCAGGGTGATGTGGGCCTGGCCATGGGCAAGCTCTACGCCAACGACTTCAGCCAG  
 721 -----+-----+-----+-----+-----+-----+-----+  
 F T Q G D V G L A M G K L Y G N D F S Q  
 C G P G H G Q A L R Q R L Q P D

Fig. 18A

781 ACGACCATTTCCCGCTTCGAGGCCCTCAACCTGAGCTTCAAGAACATGTGCAAACTCAAG  
 -----+-----+-----+-----+-----+-----+  
 T T I S R F E A L N L S F K N M C K L K  
 D H F P L R G P Q P E L Q E H V Q T Q A  
  
 841 CCCCTCCTGGAGAAGTGGCTCAACGATGCAGAGACTATGTCTGTGGACTCAAGCCTGCCC  
 -----+-----+-----+-----+-----+-----+  
 P L L E K W L N D A E T M S V D S S L P  
 P P G E V A Q R C R D Y V C G L K P A Q  
  
 901 AGCCCCAACCAGCTGAGCAGCCCCAGCCTGGGTTTCGAGCCTGCCGGCCGGAGACGCAAG  
 -----+-----+-----+-----+-----+-----+  
 S P N O L S S P S L G F E P A G R R R K  
 P Q P A E Q P Q P G F R A C M P E T Q E  
  
 961 AAGAGGACCAGCATCGAGACAAACGTCCTCGCCTTAGAGAAGAGTTTCTAGCGAAC  
 -----+-----+-----+-----+-----+-----+  
 K R T S I E T N V R F A L E K S F L A N  
 E D Q M R D K R P L R L R E E F S S E P  
  
 1021 CAGAAGCCTACCTCAGAGGAGATCCTGCTGATCGCCGAGCAGCTGCACATGGAGAAGGAA  
 -----+-----+-----+-----+-----+-----+  
 Q K P T S E E I L L I A E Q L H M E K E  
 E A Y L R G D P A D R R A A A H G E G S  
  
 1081 GTGATCCGCGTCTGGTTCTGCAACCGGCCCCAGAAGGACAAACGCATCAACCCCTGCAGT  
 -----+-----+-----+-----+-----+-----+  
 V I R V W F C N R R Q K E K R I H P C S  
 D P R L V L Q P A P E G E T H Q P L Q C  
  
 1141 GCGGCCCCCATGCTGCCCAGCCCAGGGAAGCCGGCCAGCTACAGCCCCCATATGGTCACA  
 -----+-----+-----+-----+-----+-----+  
 A A P M L P S P G K P A S Y S P H H V T  
 G P H A A Q P R E A G Q L Q P P Y G H T  
  
 1201 CCCCAGGCGGCGGGGACCTTACCGTTGTCCCAAGCTTCCAGCAGTCTGAGCACAACA  
 -----+-----+-----+-----+-----+-----+  
 P Q G G A G T L P [L] S Q A S S S [L] S T T  
 P A G R G D L T V V P S F Q Q S E H N S

Fig. 18A  
(CONTINUED)

GTTACTACCTTATCCTCAGCTGTGGGGACGCTCCACCCCAGCCGGACAGCTGGAGGGGGT  
 1261 -----+-----+-----+-----+-----+-----+-----+  
 V T T [L] S S A V G T [L] H P S R T A G G G  
 Y Y L I L S C G D A P P Q P D S N M G W

GGGGGCGGGGGCGGGGCTGCGCCCCCTCAATTCCATCCCCTCTGTCACTCCCCACCC  
 1321 -----+-----+-----+-----+-----+-----+-----+  
 G G G G G A A P P L N S I P S V T P P P  
 G M G R G C A P P Q F H P L C H S P T P

CCGGCCACCACCAACAGCACAAACCCAGCCCTCAAGGCAGCCACTCGGCTATCGGCTTG  
 1381 -----+-----+-----+-----+-----+-----+-----+  
 P A T T N S T N P S P Q G S H S A I G L  
 G H N Q Q H K P Q P S R Q P L G Y M L V

TCAGGCCTGAACCCCAGCACGGGGTAAGTGGGTGCACGTGGGAAGCTGTGGGGAGAAGCA  
 1441 -----+-----+-----+-----+-----+-----+-----+  
 S G L H P S T G +  
 A P E P Q N G V S G C T W E A V G R S R

GCGTCGCTGCTCCTTCTAGGGTGGGGAGCGGCACCCCAGTTATGTTGGCAGGTCCCTGCC  
 1501 -----+-----+-----+-----+-----+-----+-----+  
 V A A A S R V G S G T P V M L A G P C P

CCTGCTAATGCCTCTGCTTTGCCTCTTGCAGAAGCACAAATGGTGGGGTTGAGCTCCGGCT  
 1561 -----+-----+-----+-----+-----+-----+-----+  
 C +

GAGTCCAGCCCTCATGAGCAACAACCCTTTGGCCACTATCCAAGGTGCGTGCTGCCTCAT  
 1621 -----+-----+-----+-----+-----+-----+-----+

GTCACACCCATCGTCACCAGCCCCGGAATTCGAG  
 1681 -----+-----+-----+-----+-----+-----+

Fig. 18A  
(CONTINUED)

CCTCAAGGCAGCCACTCGGCTATCGGCTTGTTCAGGCCTGAACCCAGCACGGGCCCTGGC  
 1411 -----+-----+-----+-----+-----+-----+-----+  
 P Q G S H S A I G L S G L N P S T G P G  
 S A Q P L G Y R L V M P E P Q M G P N P

CTCTGGTGGAACCCTGCCCCCTTACCAGCCTTGATGGCAGCGGGAATCTGGTGCTGGGGGC  
 1471 -----+-----+-----+-----+-----+-----+-----+  
 L W W N P A P Y Q P .  
 L V E P C P L P A L M A A G I W C W G Q

AGCCGGTGCAGCCCCGGGGAGCCCTGGCCTGGTGACCTCGCCGCTCTTCTGAATCATGC  
 1531 -----+-----+-----+-----+-----+-----+-----+  
 P V Q P R G A L A W .

TGGGCTGCCCCCTGCTCAGCACCCCGCCTGGTGTGGGCCTGGTCTCAGCAGCGGCTGCGGG  
 1591 -----+-----+-----+-----+-----+-----+-----+

TGTGGCAGCCTCCATCTCCAGCAAGTCTCCTGGCCTCTCCTCCTCATCCTCTTCATCCTC  
 1651 -----+-----+-----+-----+-----+-----+-----+

ATCCTCCTCCTCCTCCACTTGCAGCGAGACGGCAGCACAGACCCTGGAGGTCCAGGGGGG  
 1711 -----+-----+-----+-----+-----+-----+-----+

CCCGAGGCAGGGTCCAAACCTGAGTGAGGGCCAGCCATGCCTCCCCTCCCATTCTCTGG  
 1771 -----+-----+-----+-----+-----+-----+-----+

TCCCTGCCCCGGAATTC  
 1831 -----+-----

Fig. 18B

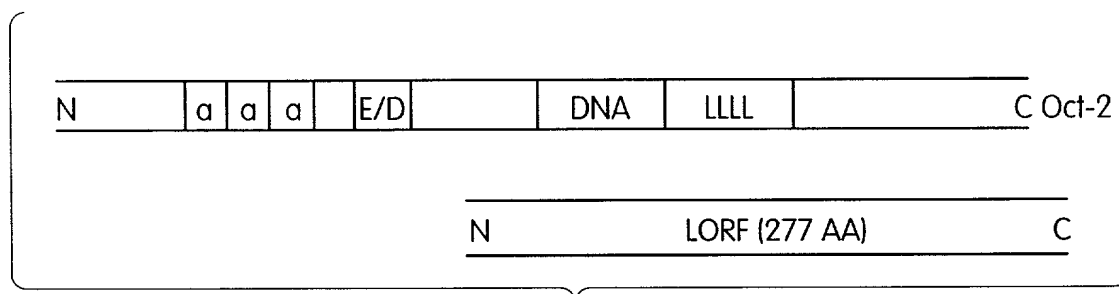


Fig. 18C

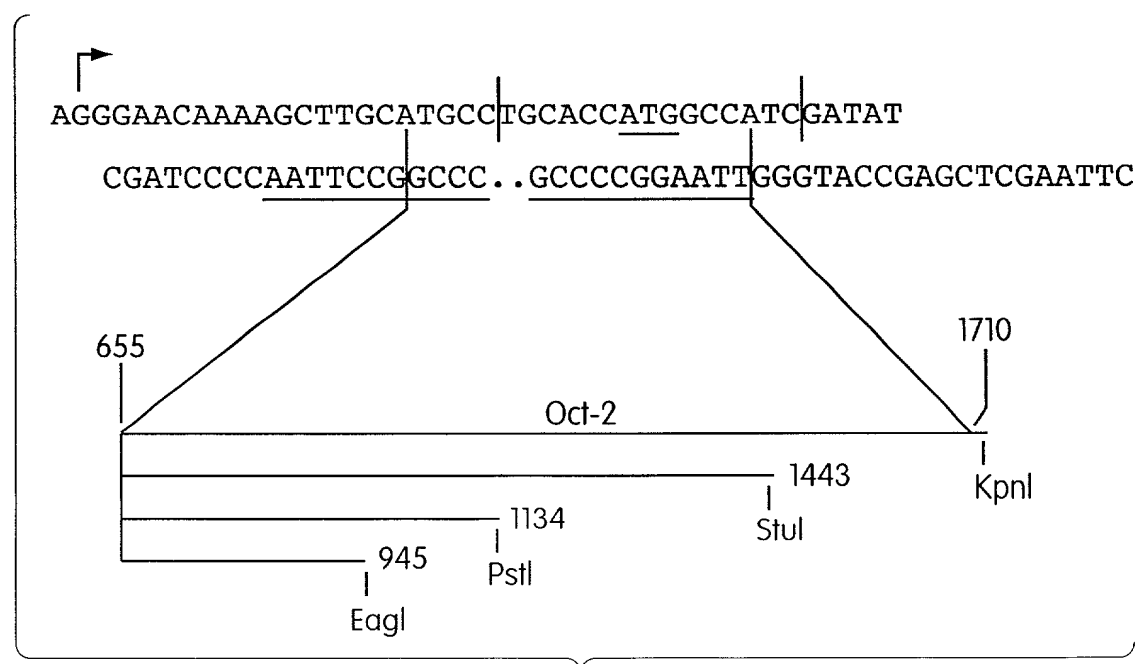


Fig. 19

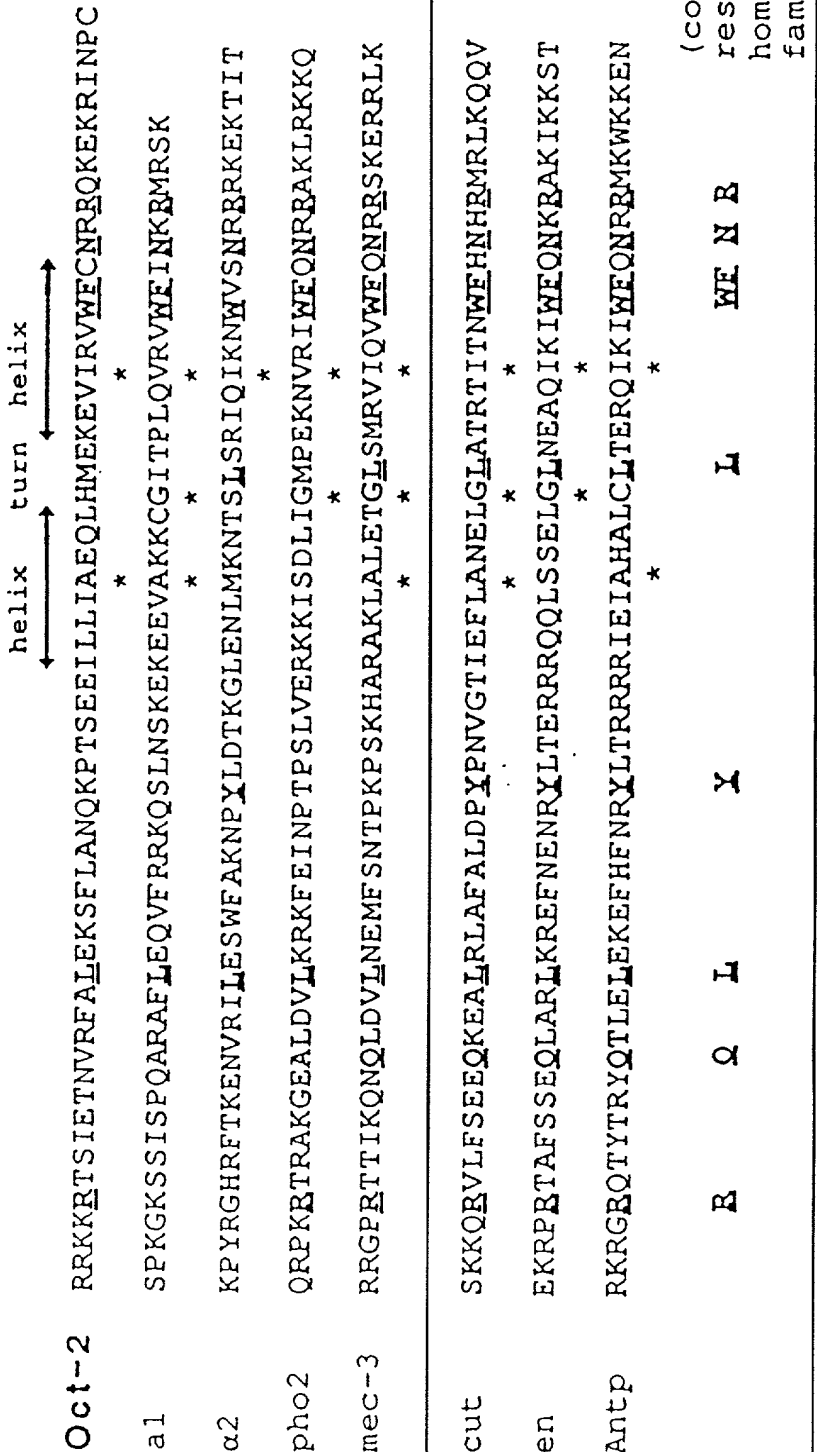


Fig. 20

Figure 21A

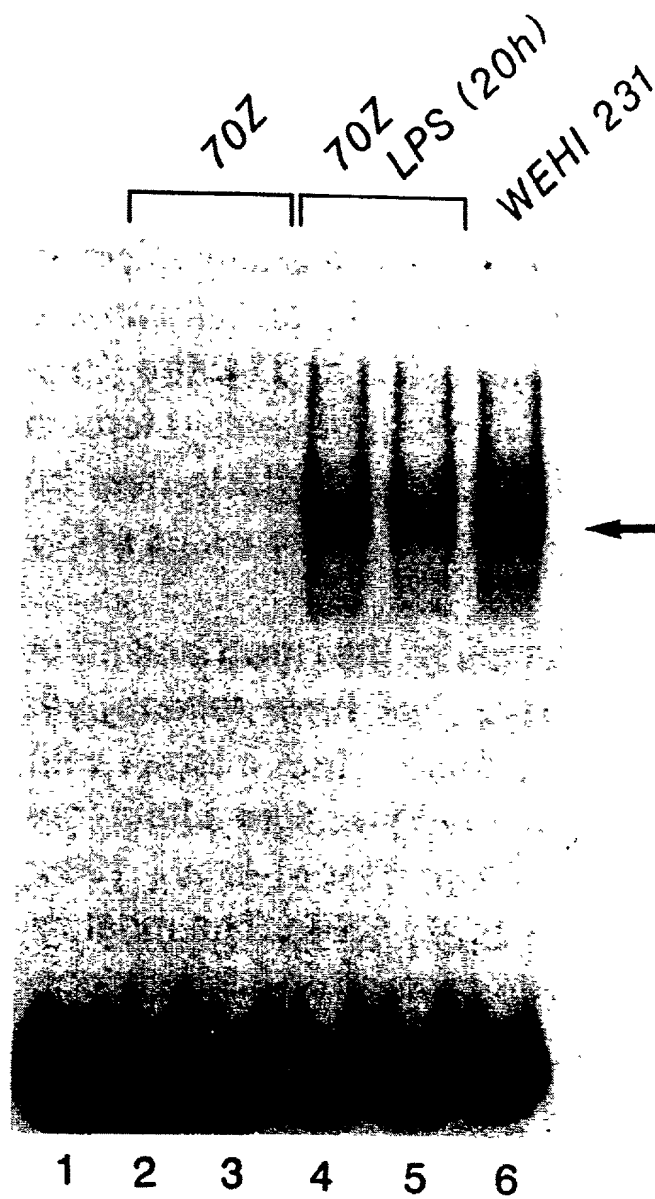


Figure 21B

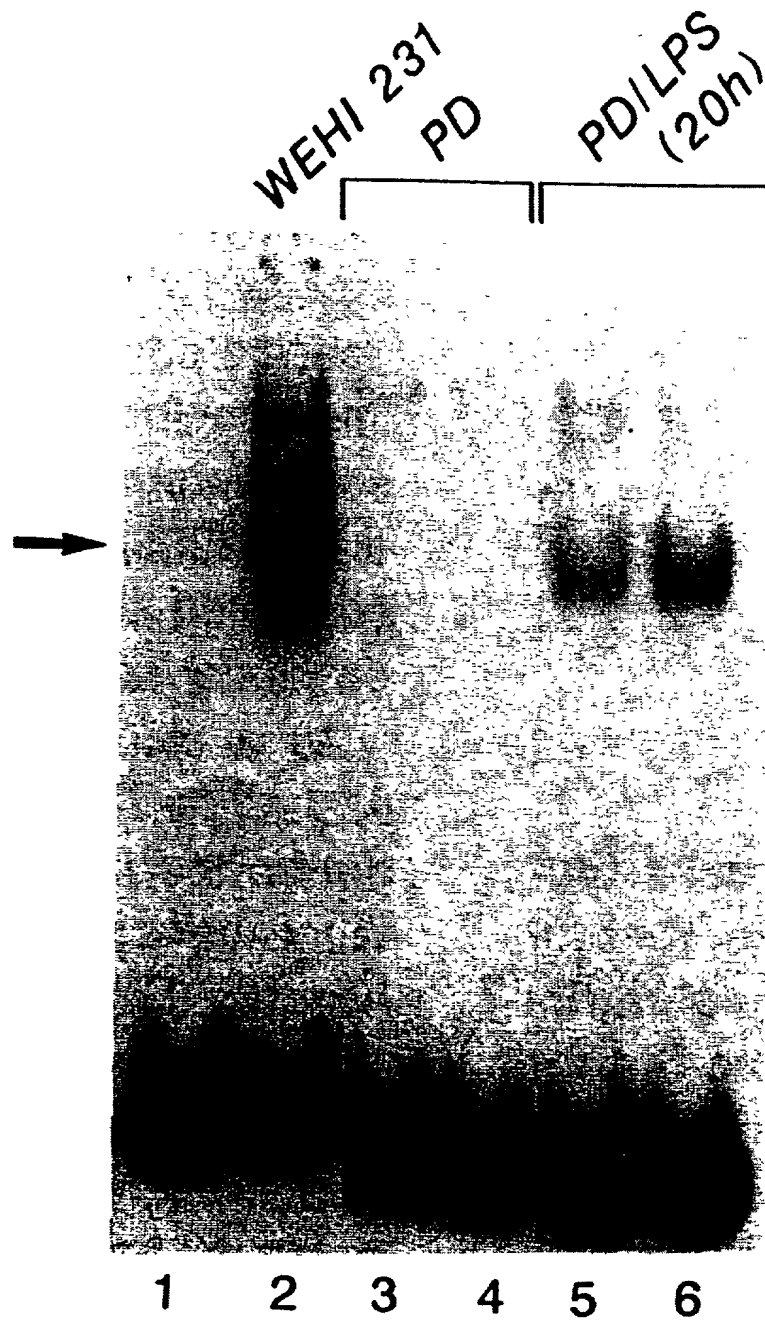




Figure 22A

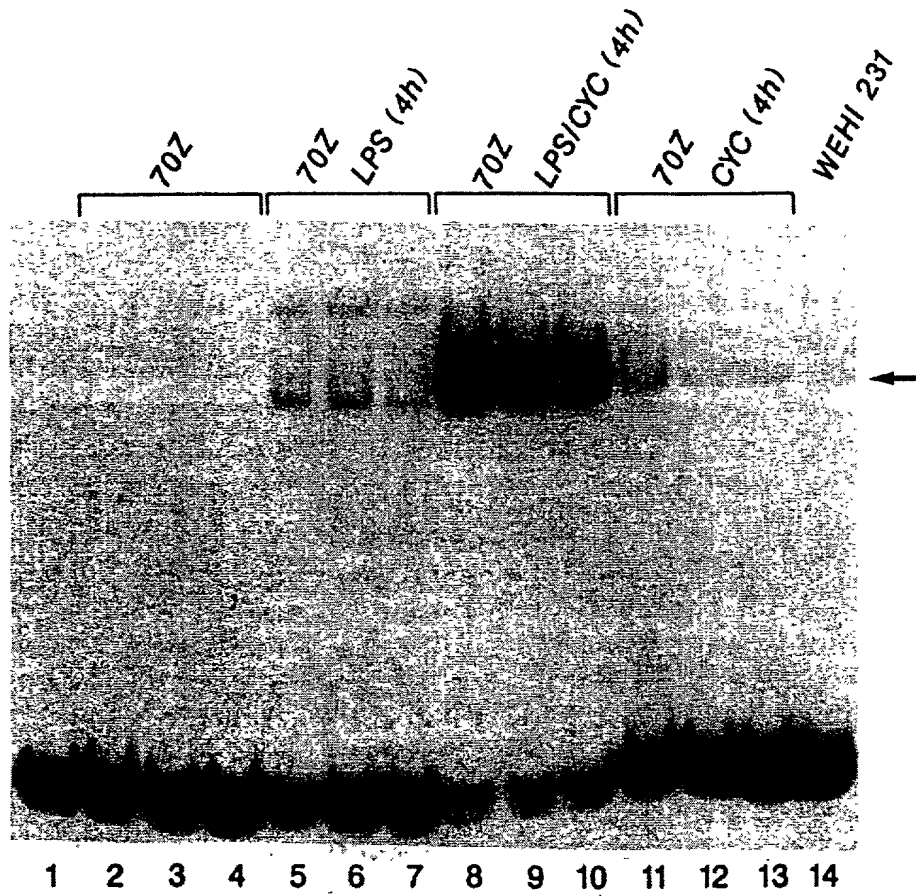


Figure 22B

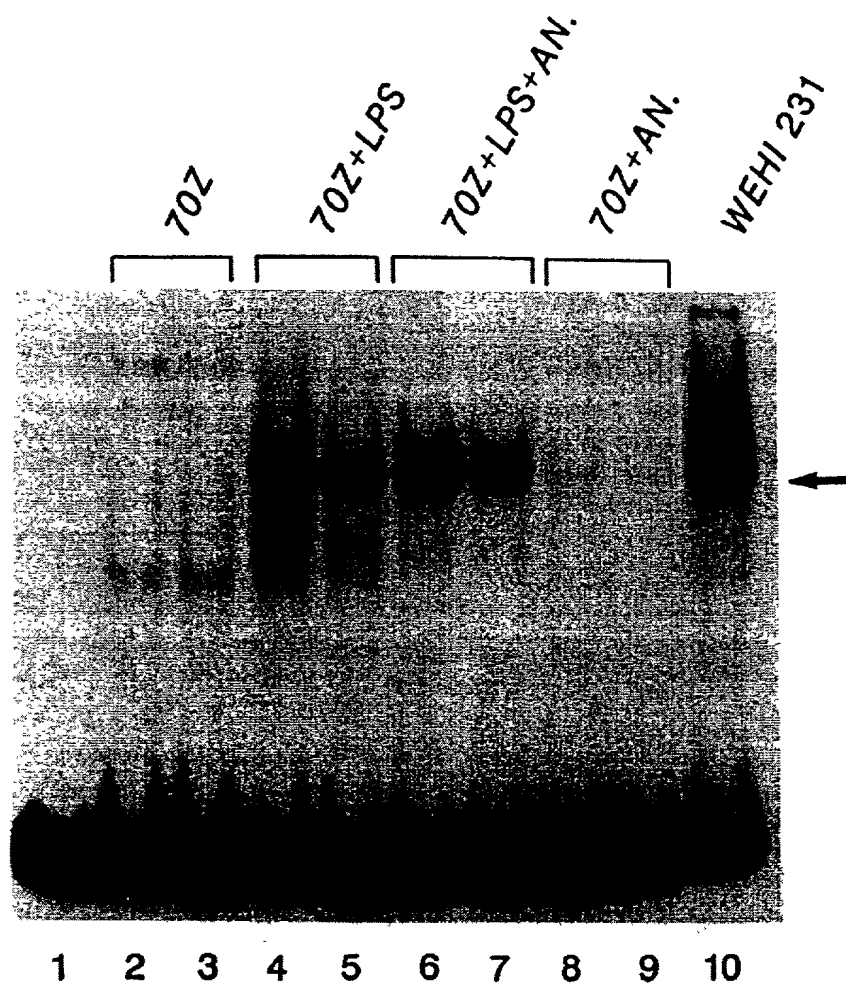


Figure 23A

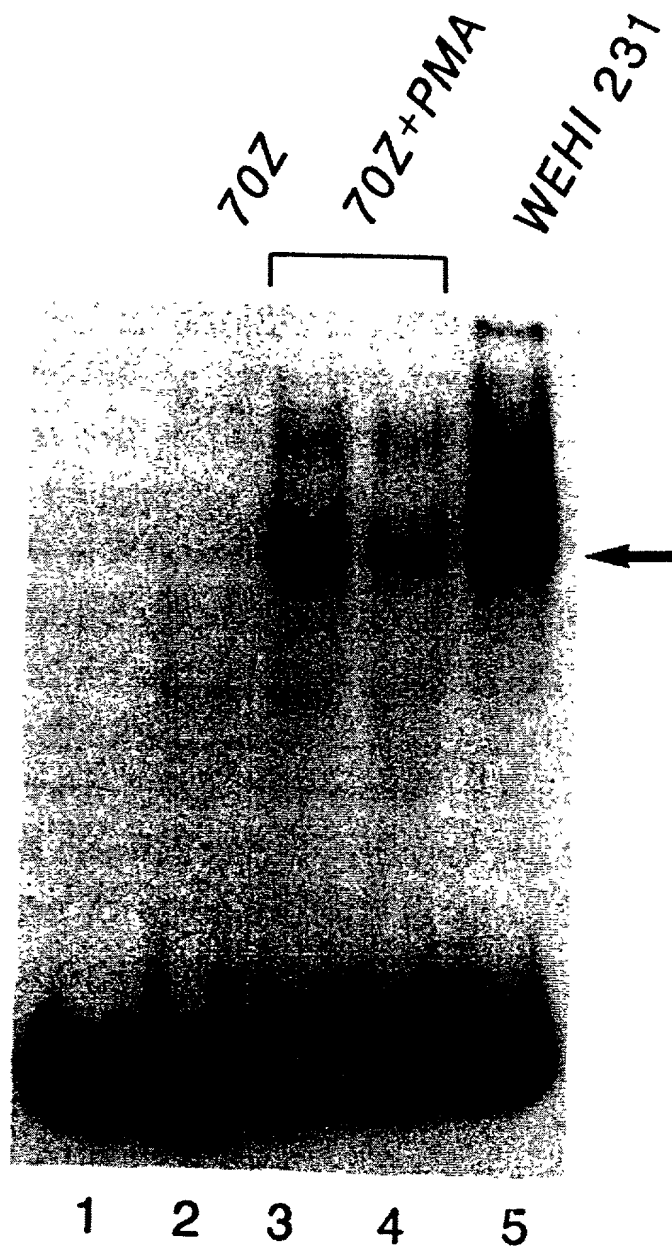


Figure 23B

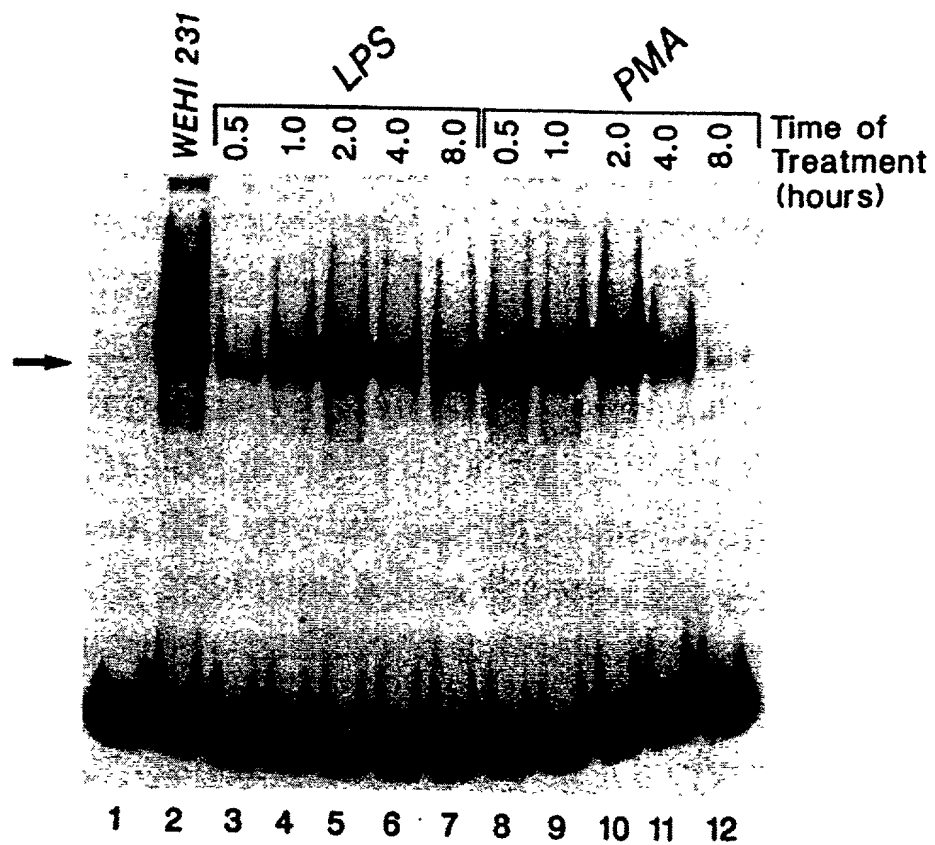


Figure 24A

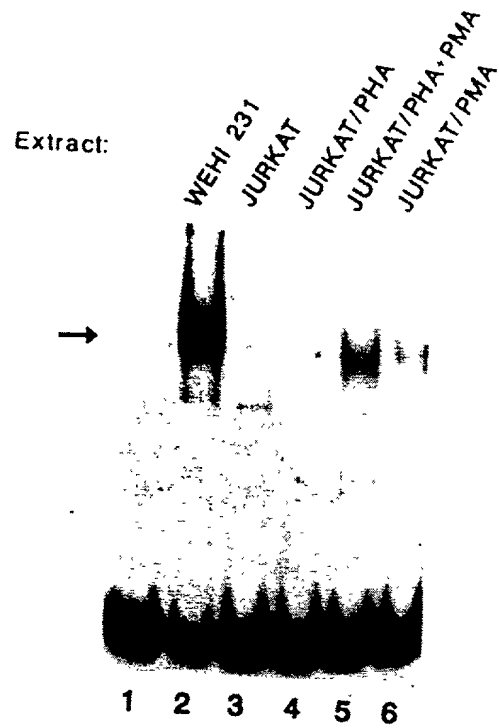


Figure 24B

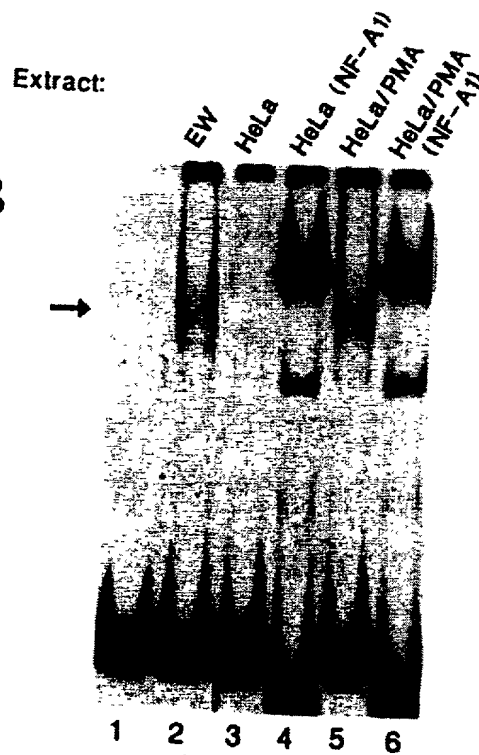
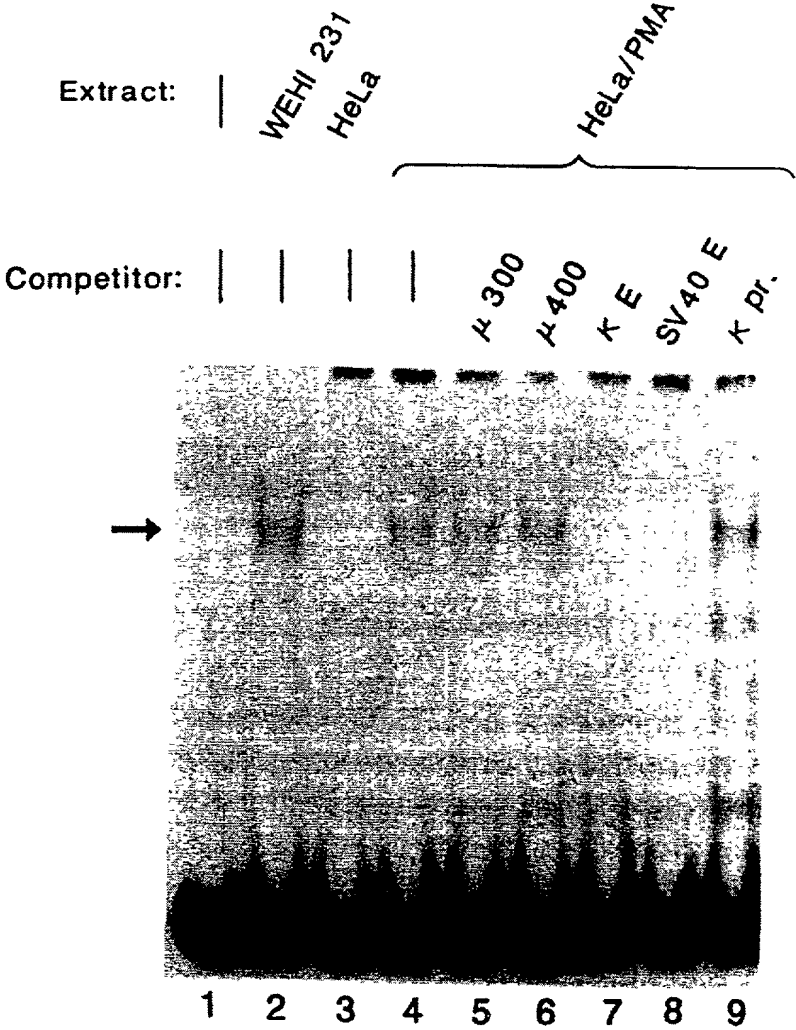


Figure 24C



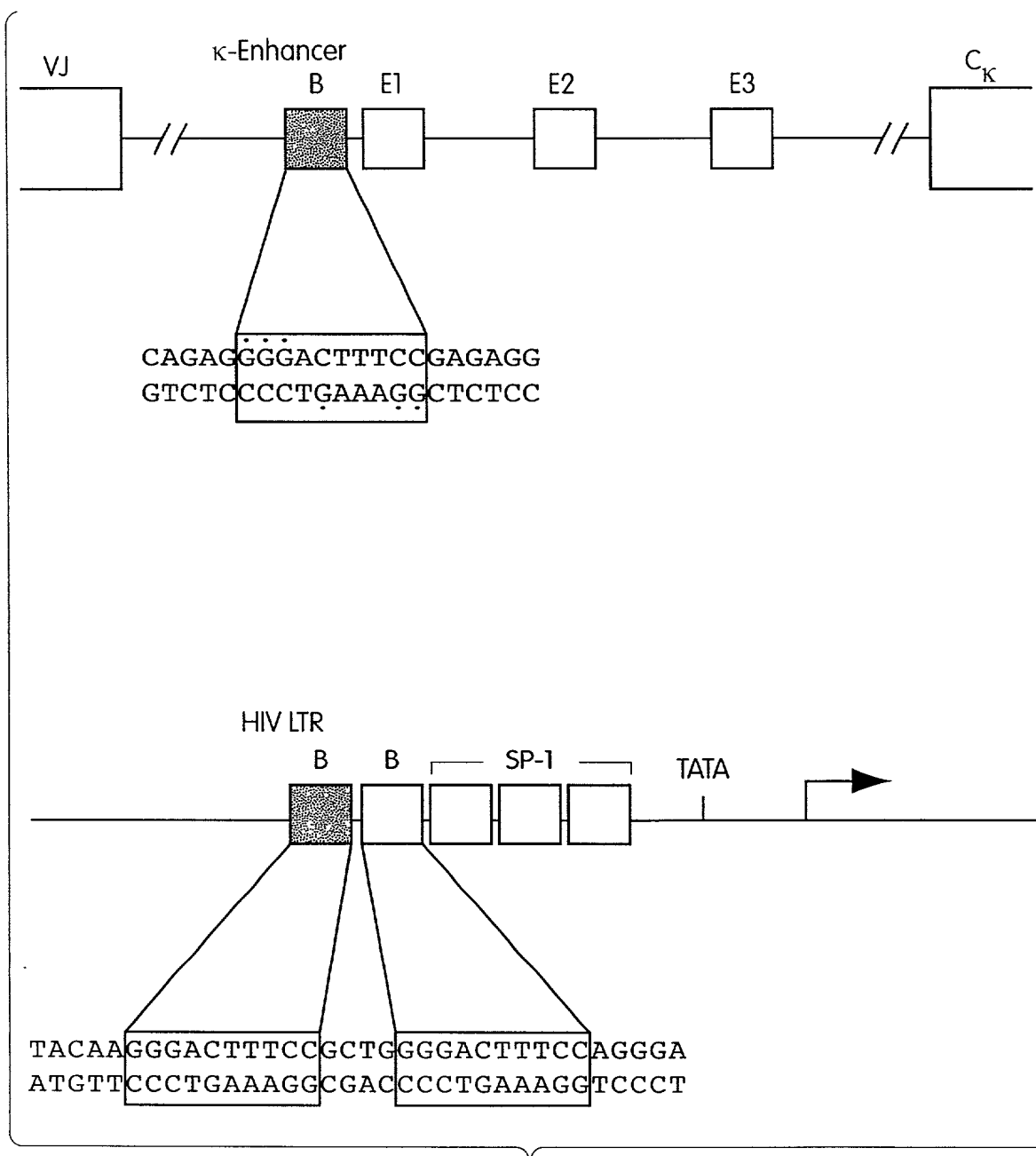
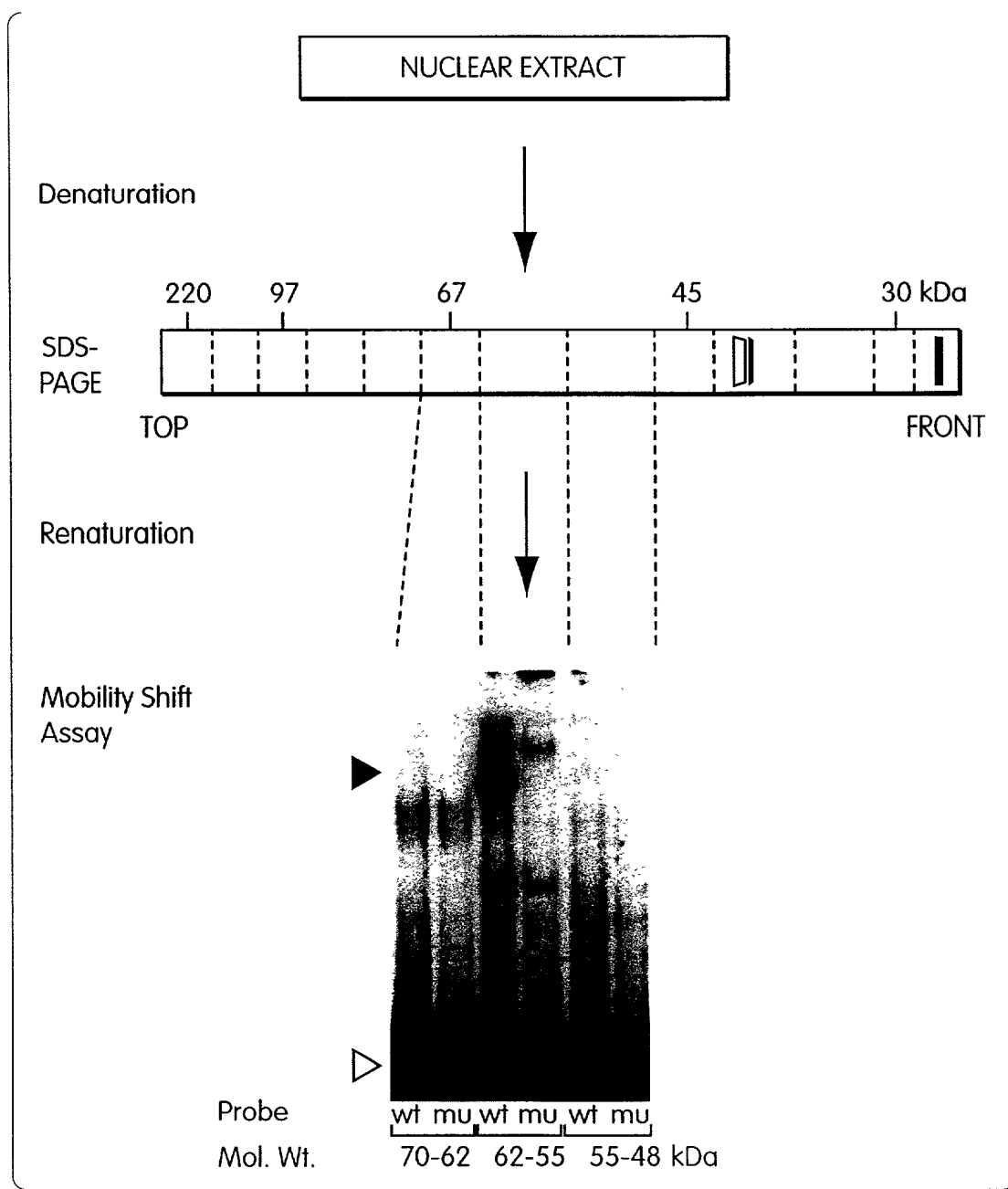


Fig. 25





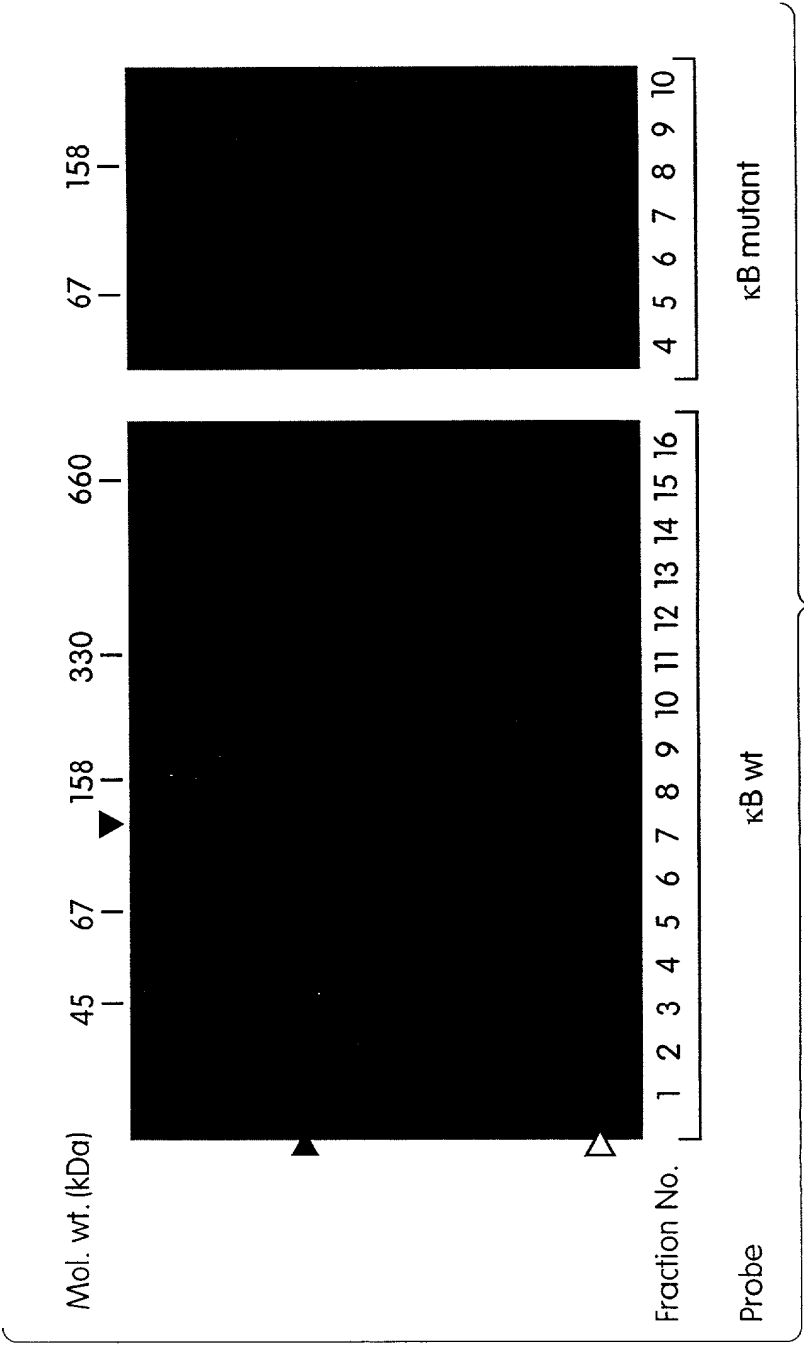


Fig. 26B

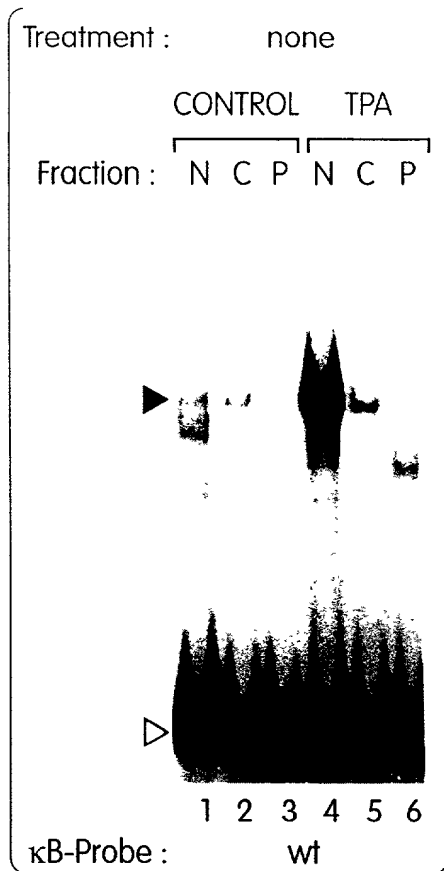


Fig. 27A

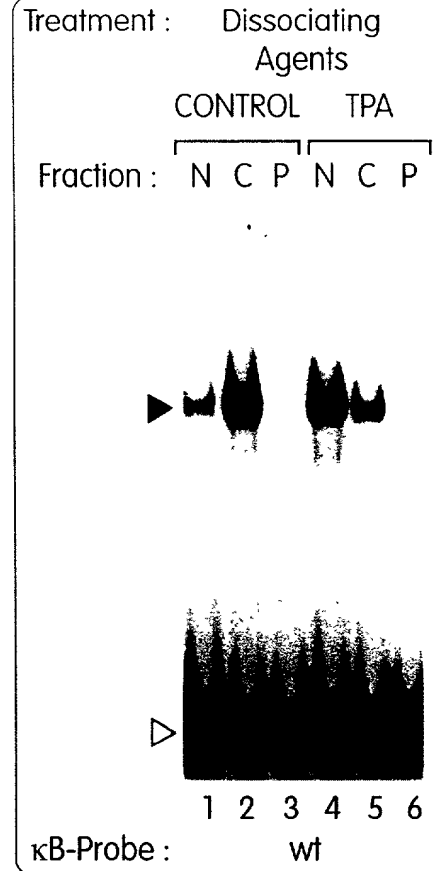


Fig. 27B

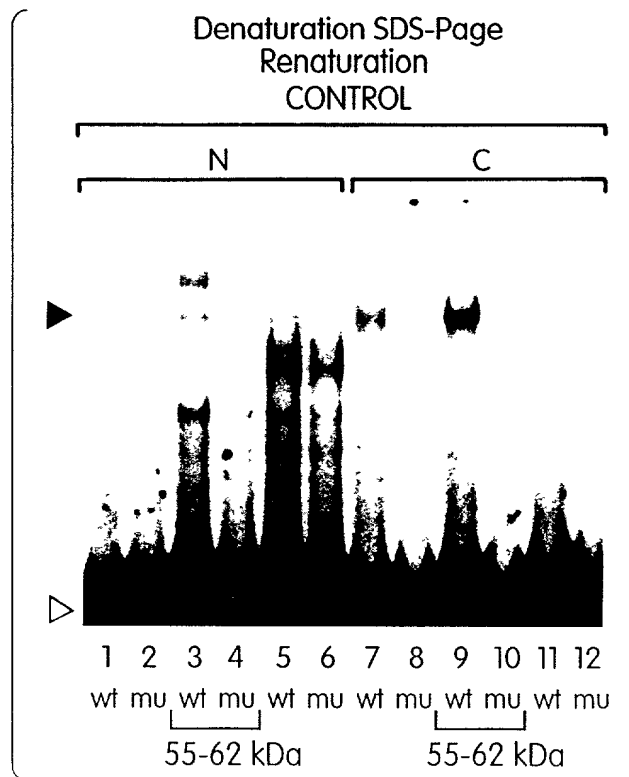


Fig. 27C

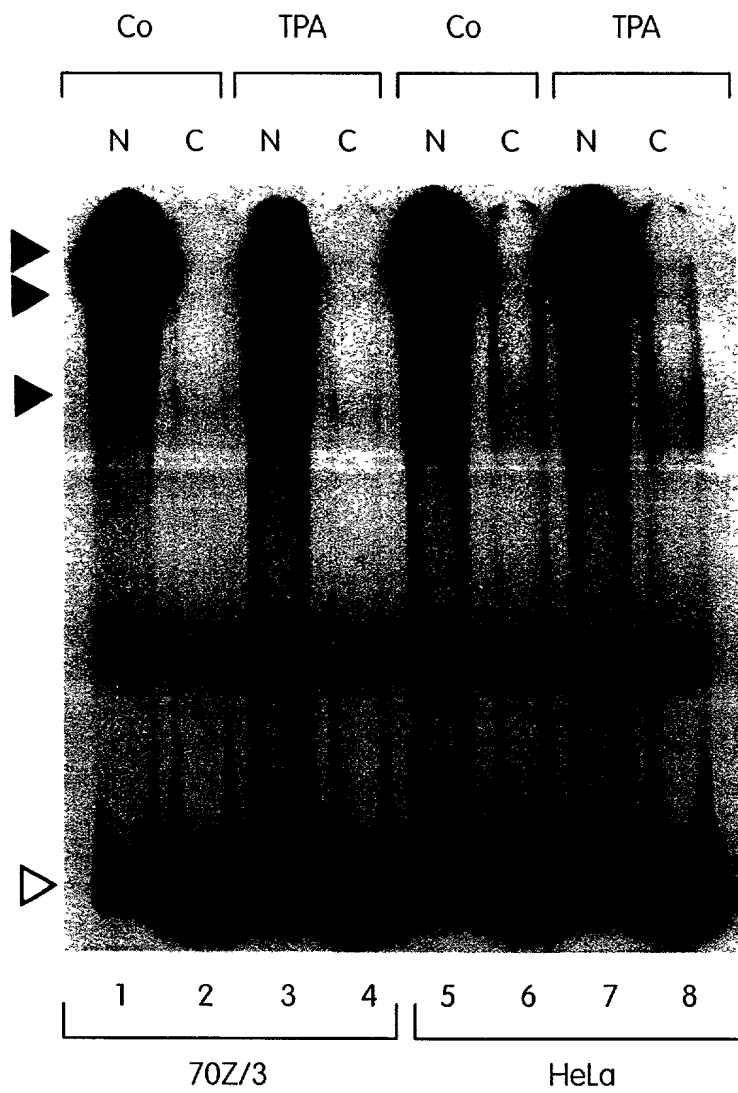


Fig. 28

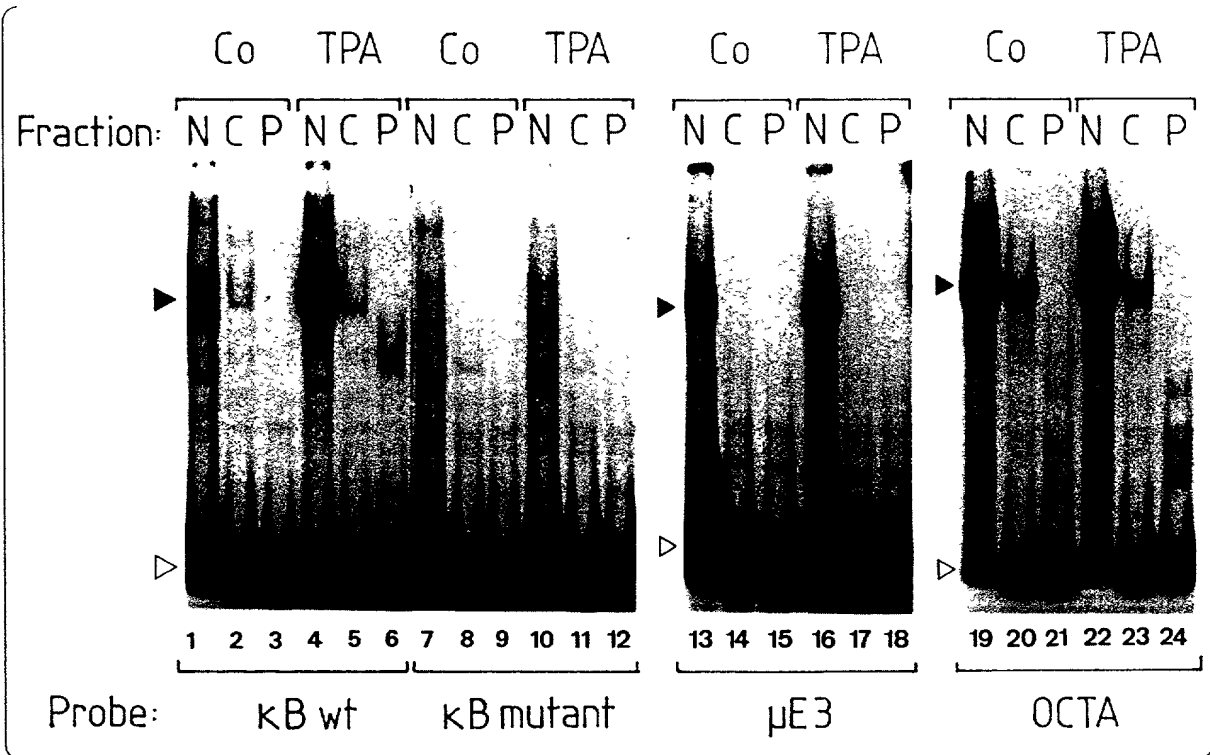


Fig. 29

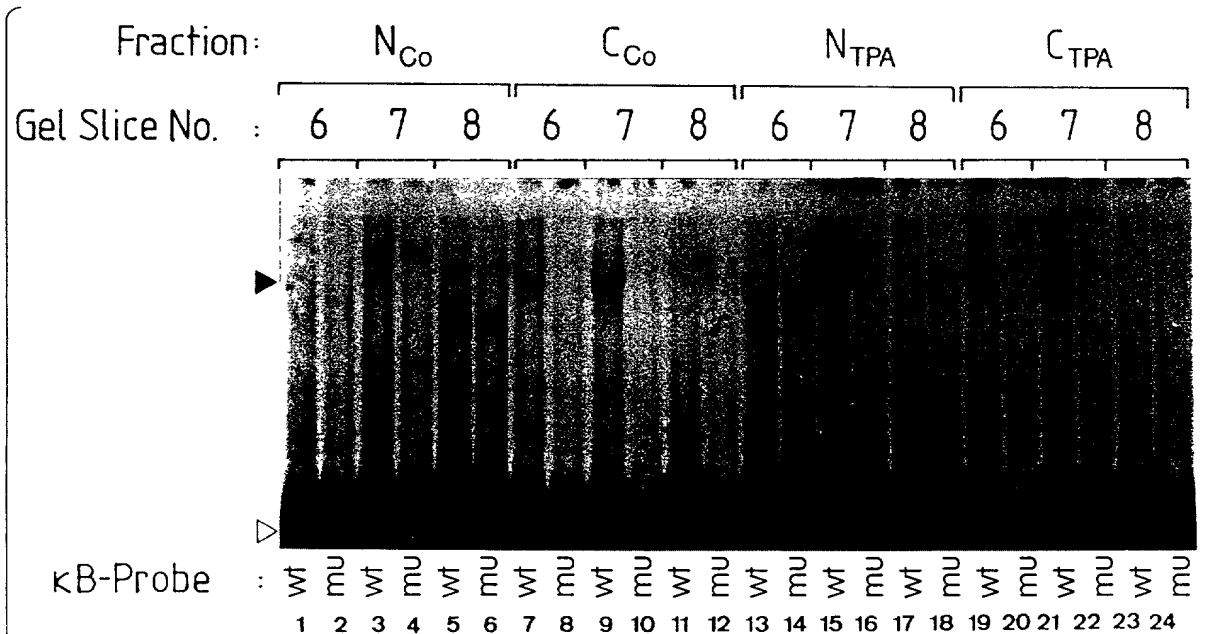
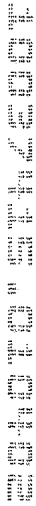
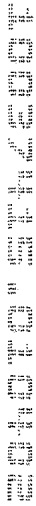


Fig. 30

[illegible][illegible]

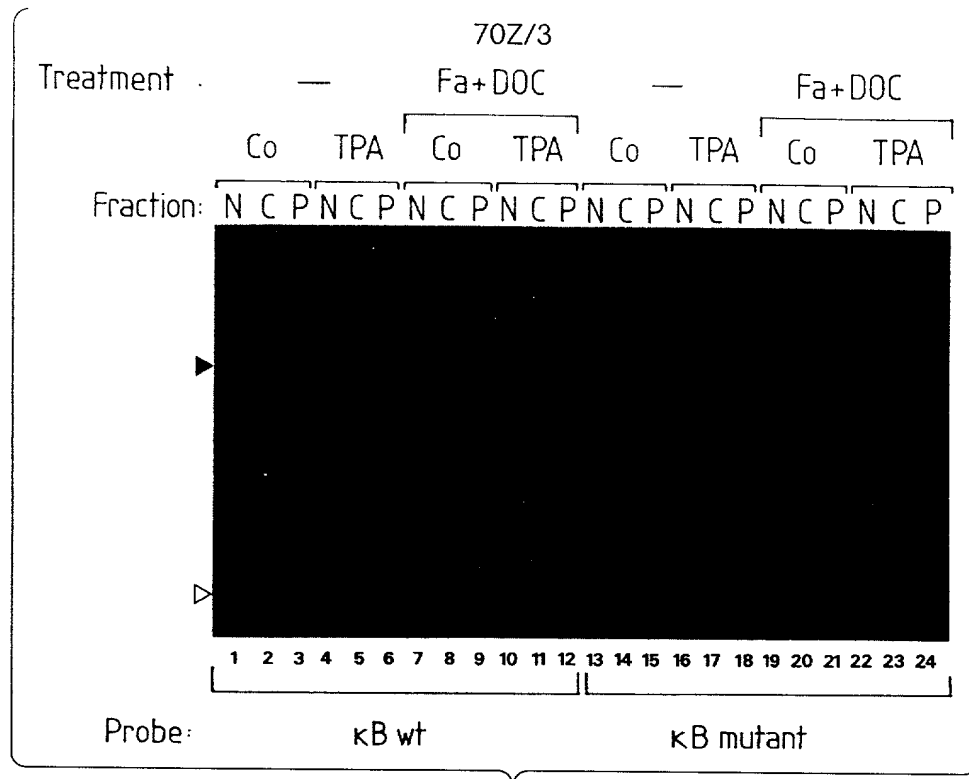


Fig. 32

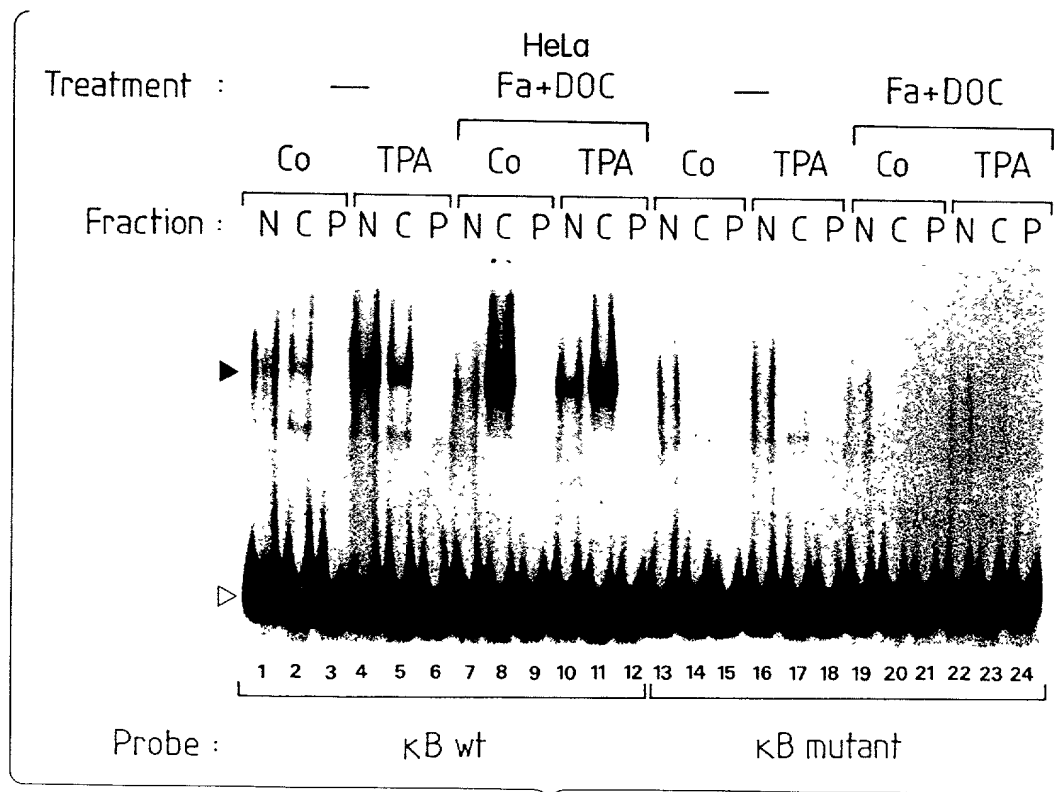


Fig. 33

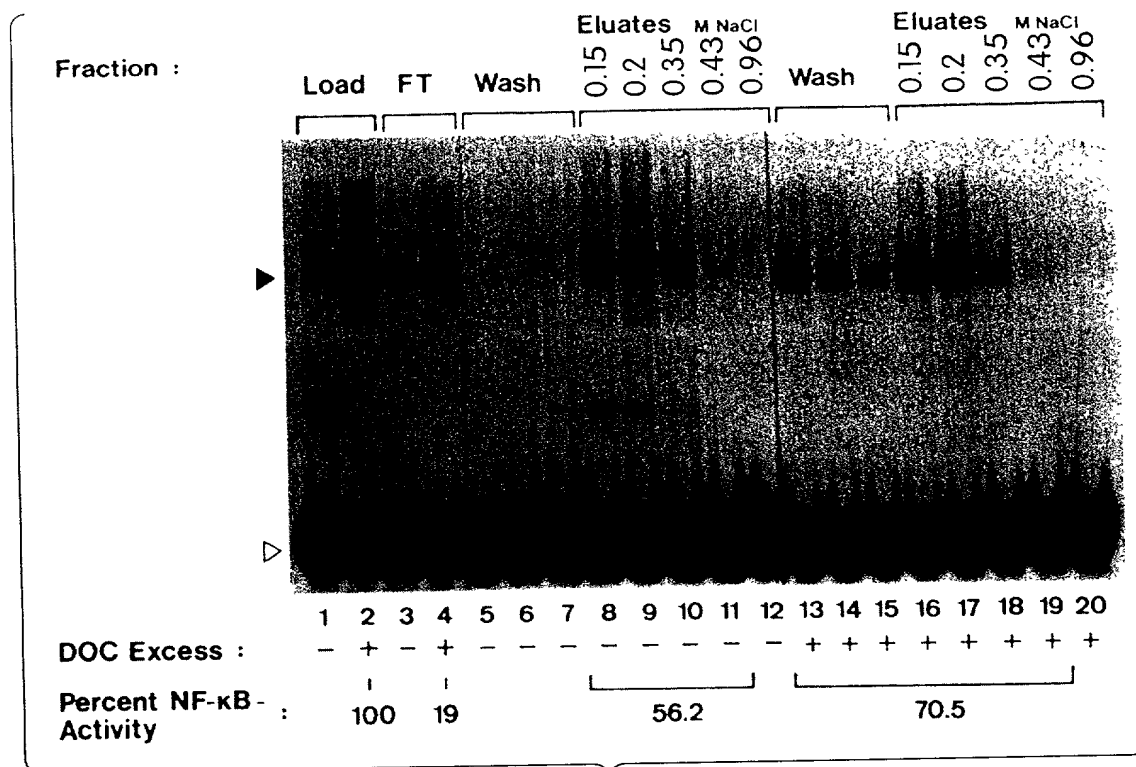


Fig. 34A

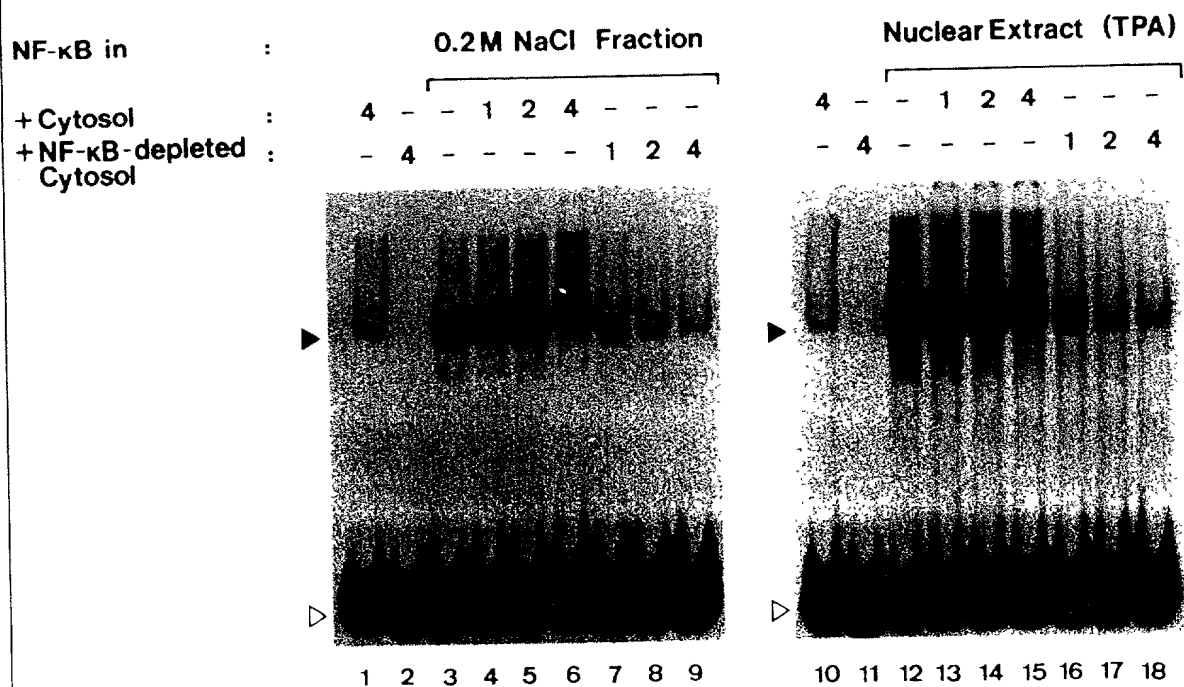


Fig. 34B

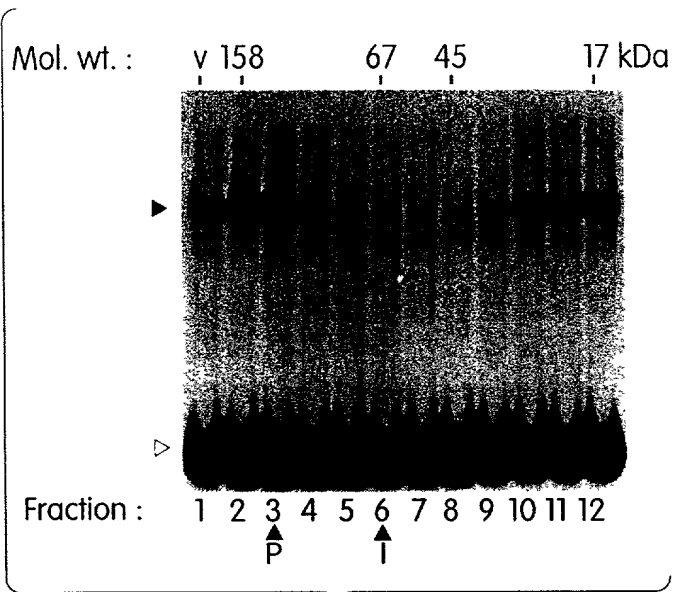


Fig. 35A

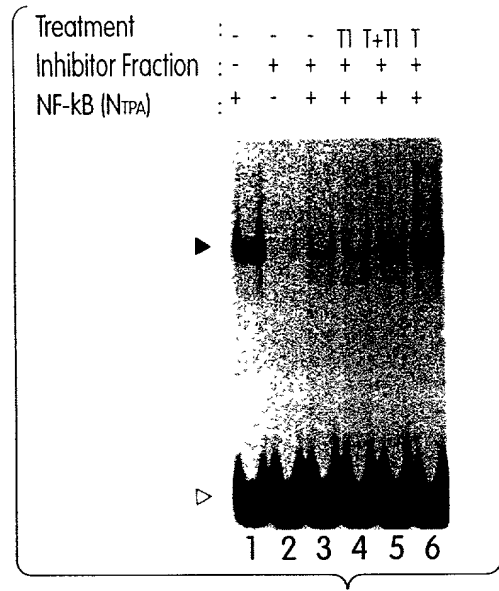


Fig. 35B

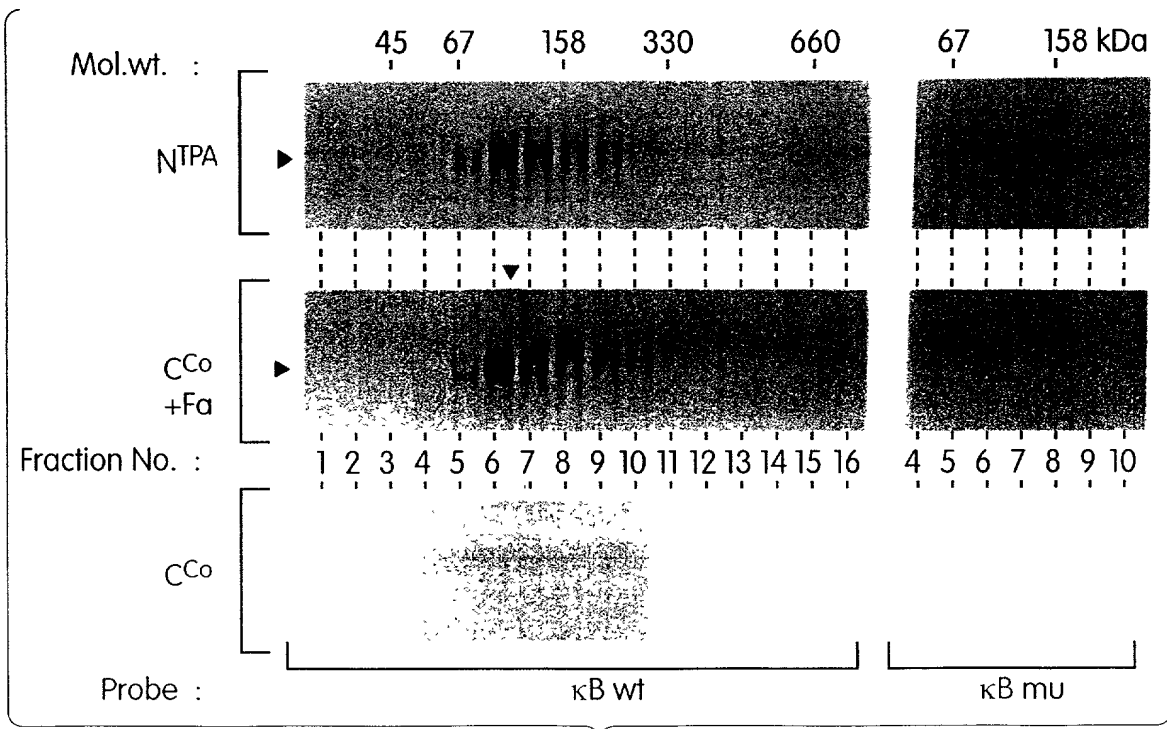


Fig. 35C



49/56

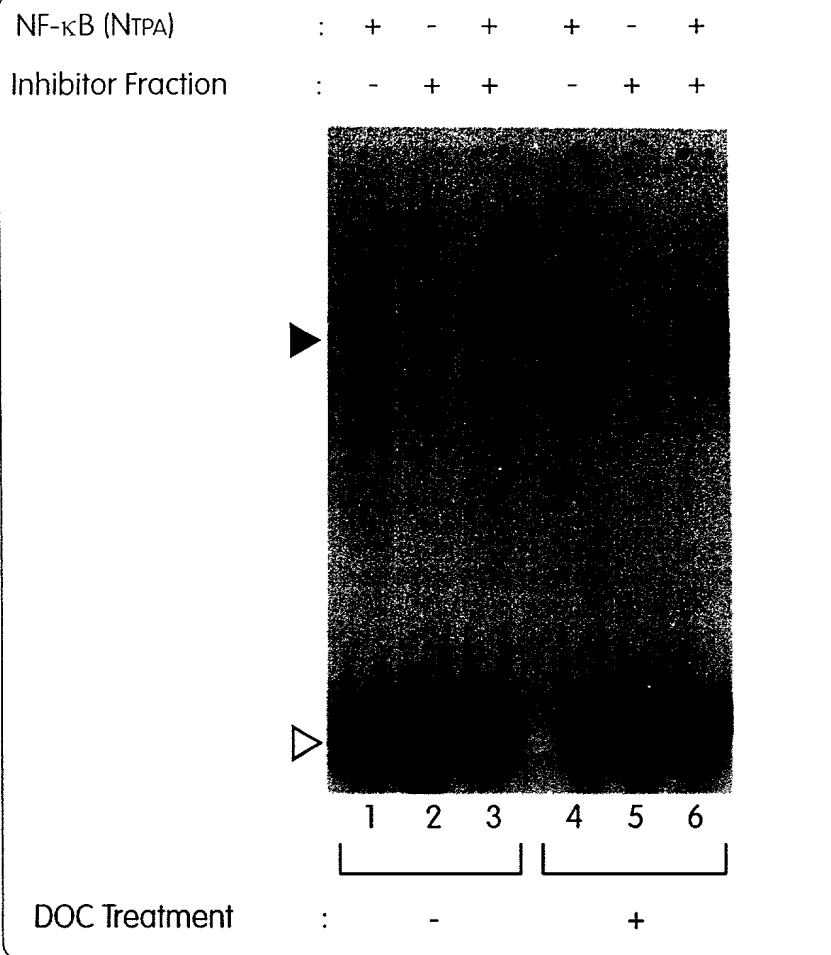


Fig. 36A

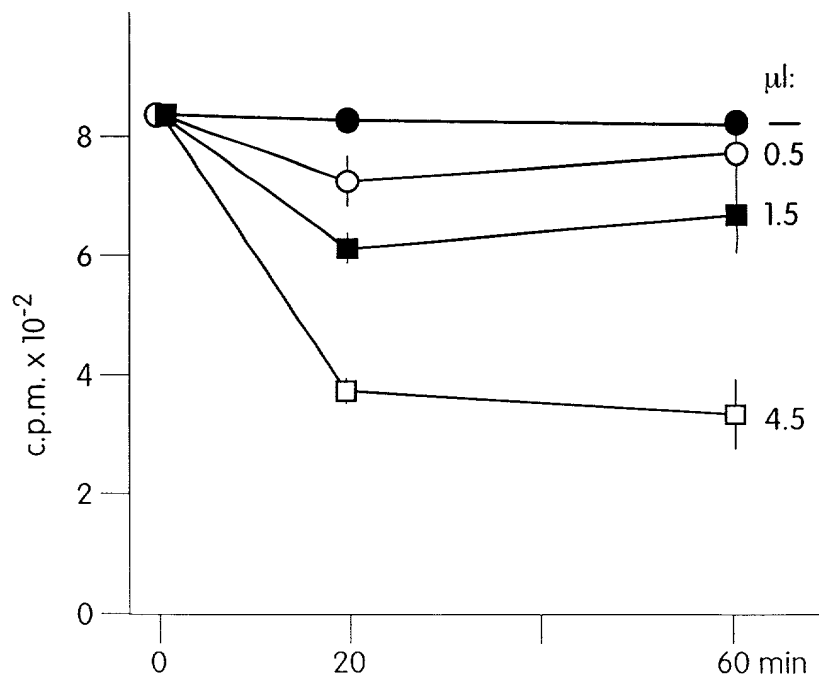


Fig. 36B

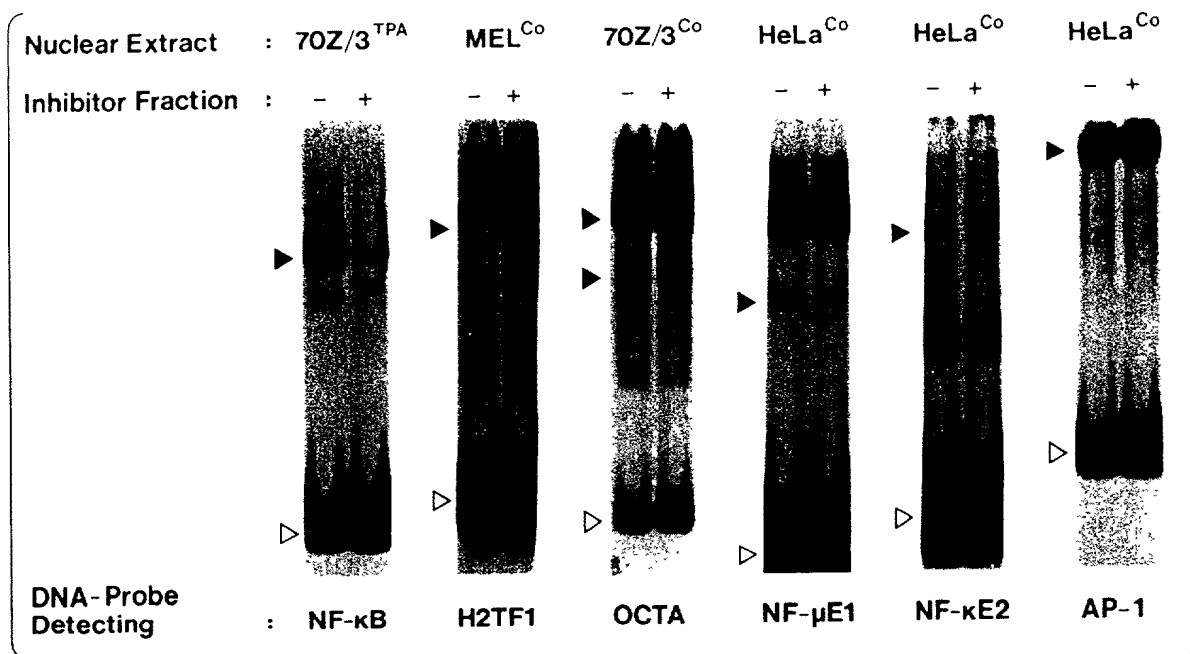


Fig. 37A

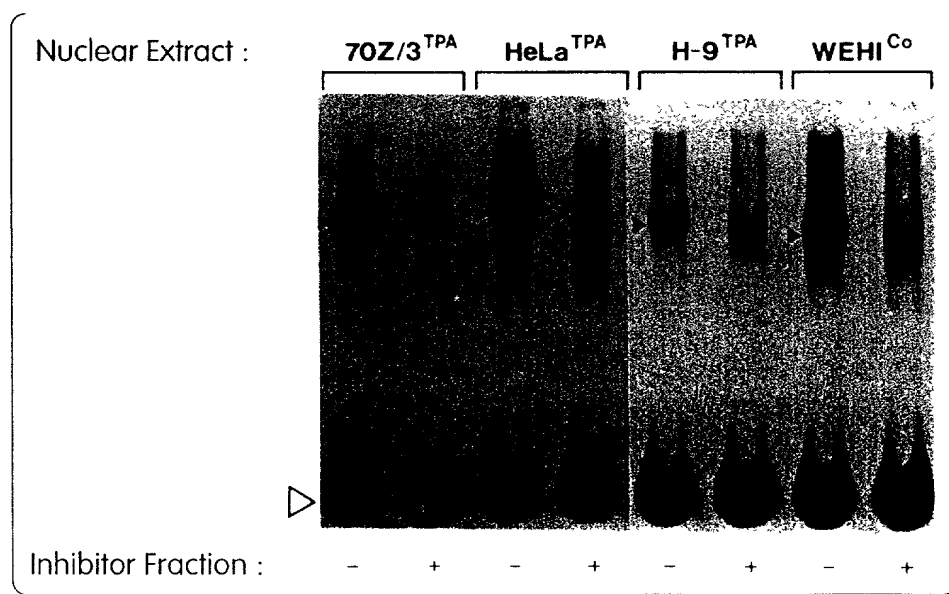


Fig. 37B

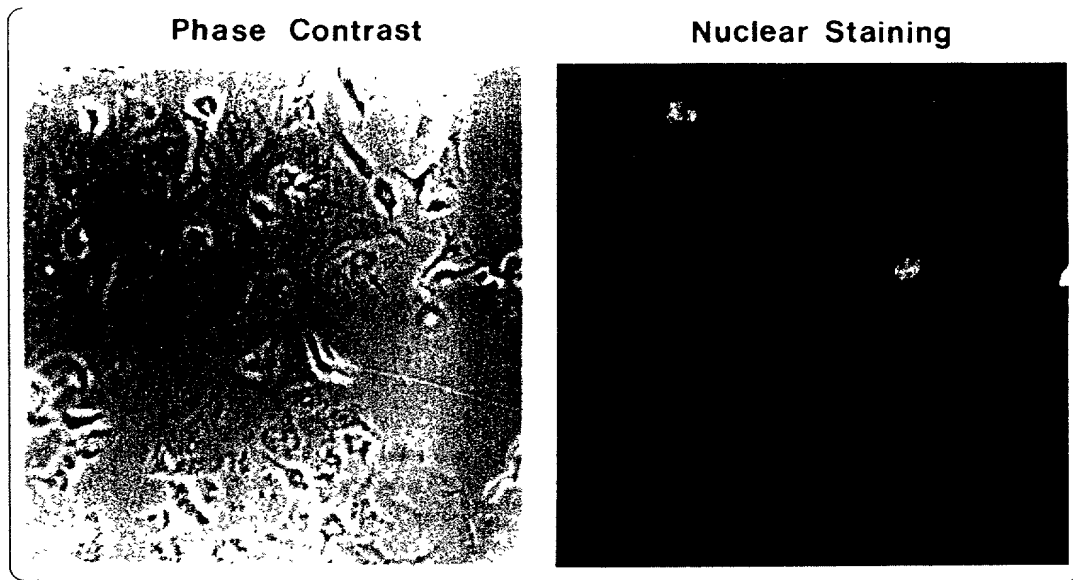


Fig. 38A

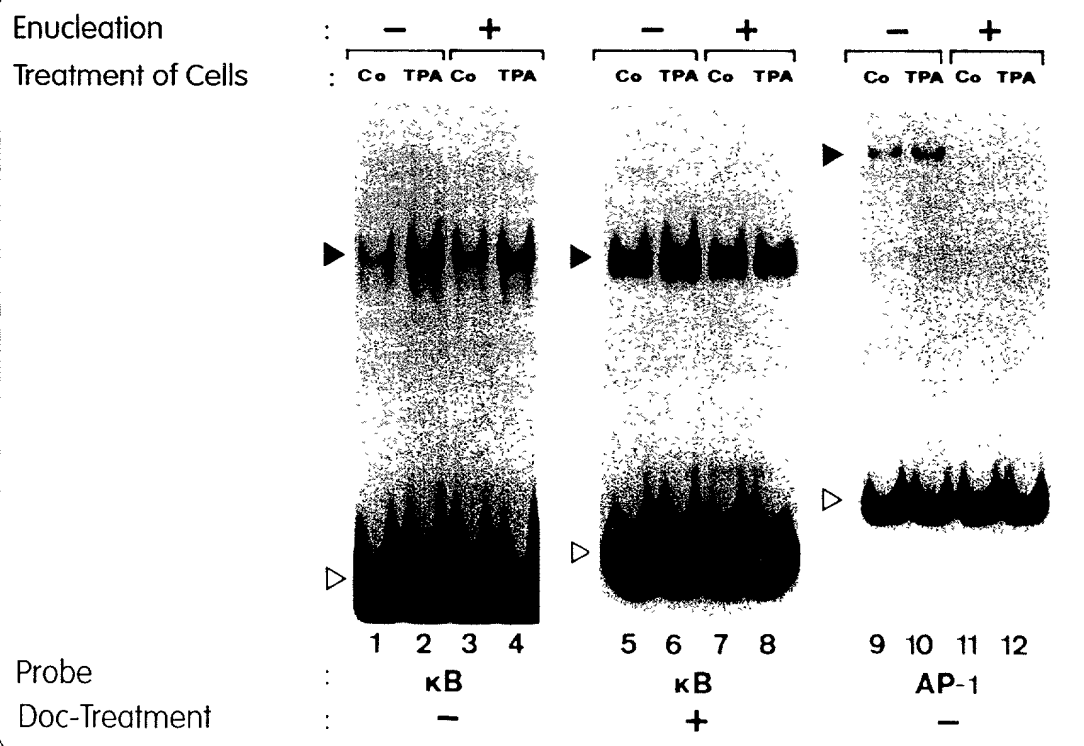


Fig. 38B

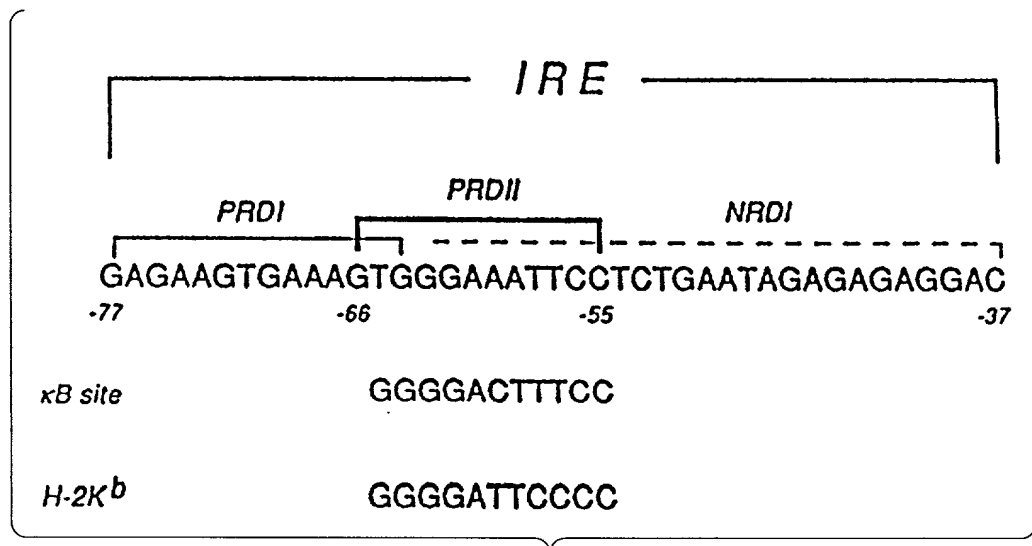


Fig. 39

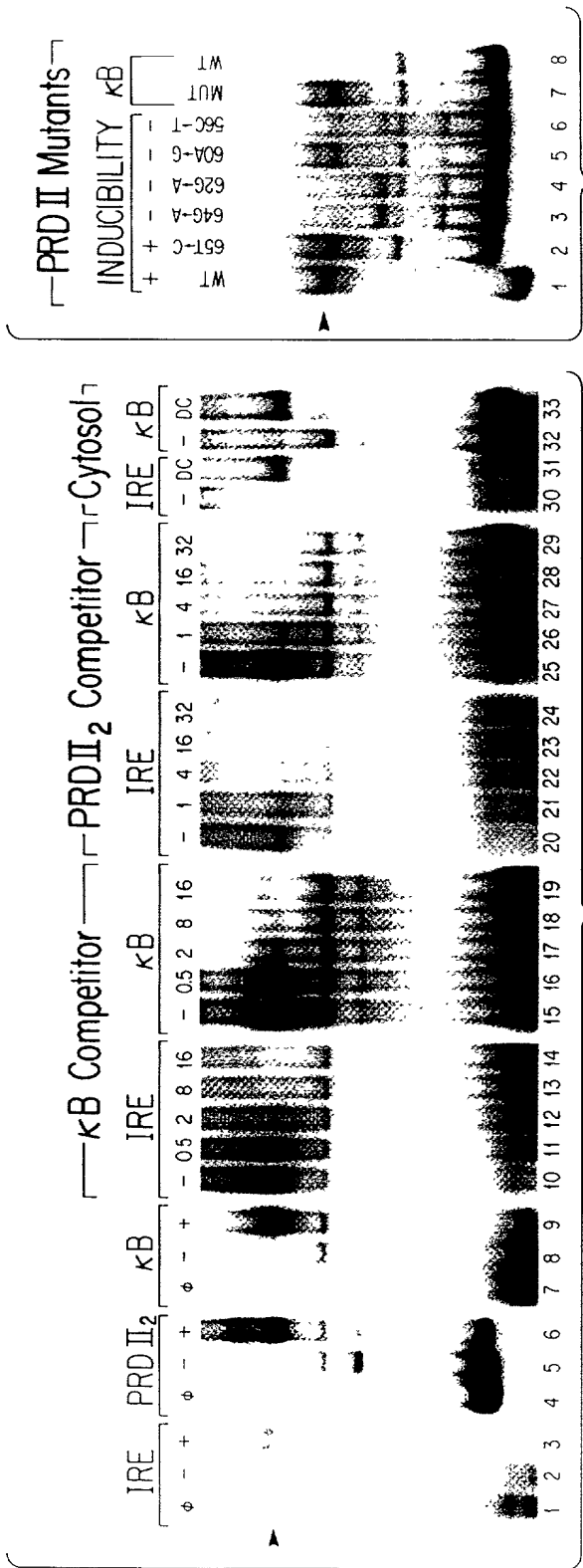


Fig. 40A

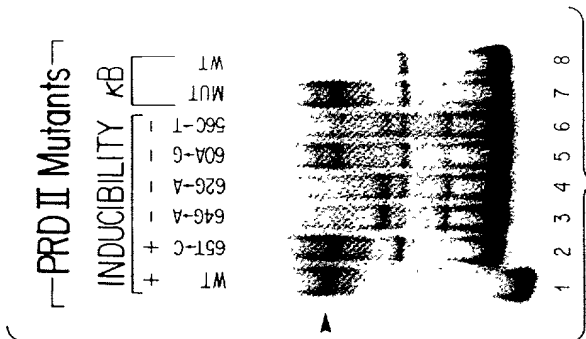


Fig. 40B

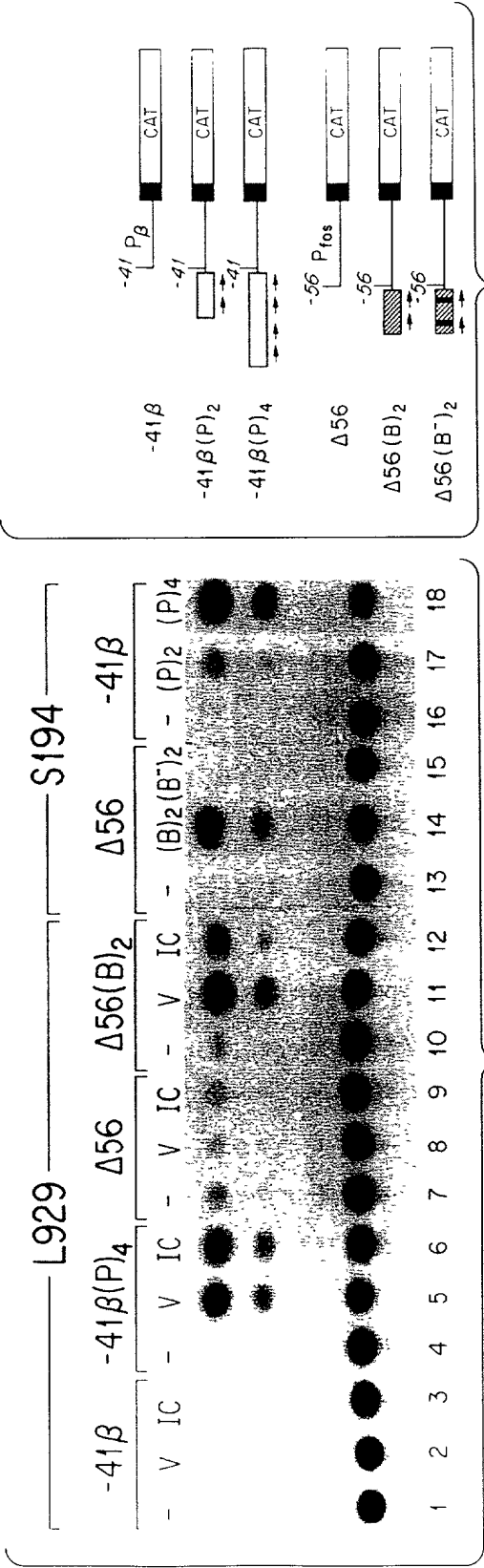


Fig. 41B

Fig. 41A

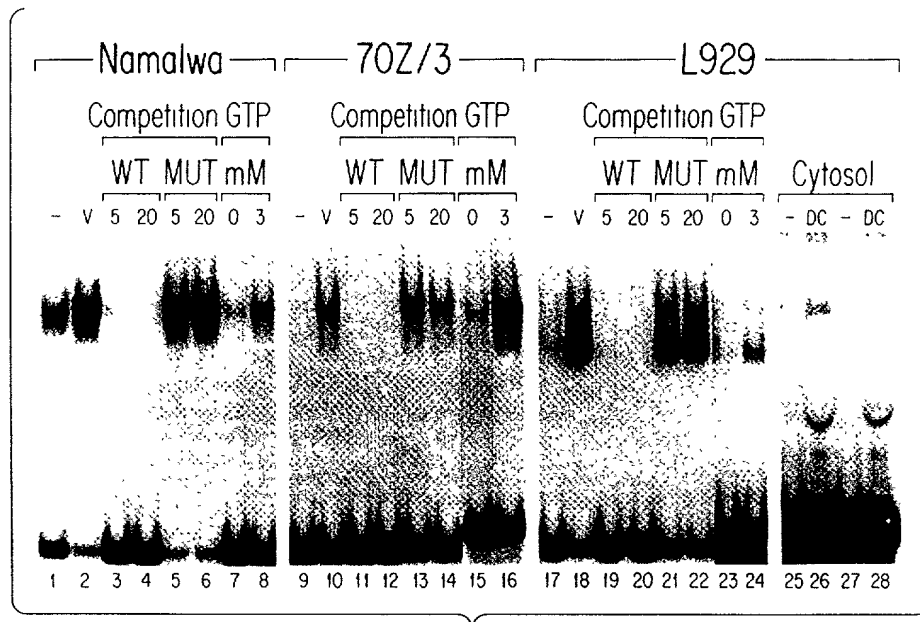


Fig. 42A

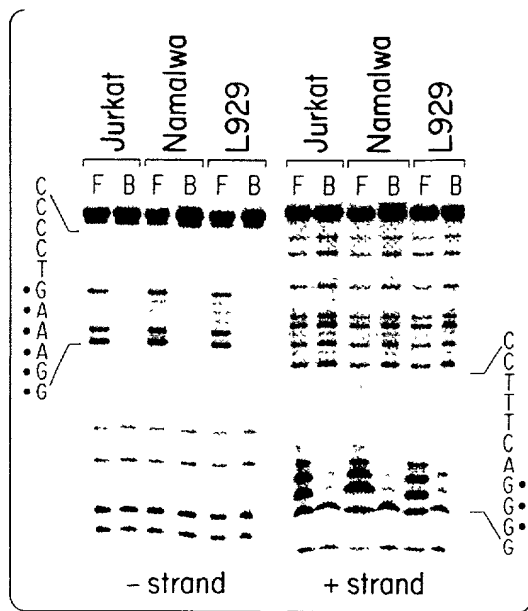


Fig. 42B

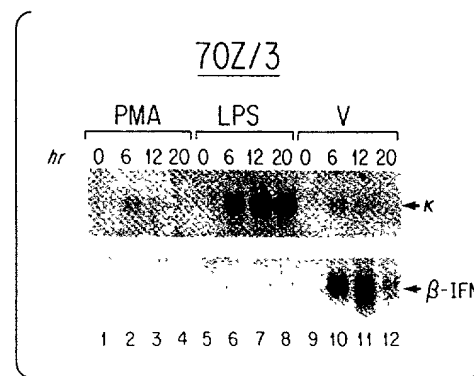


Fig. 42C





Figure 43 (continued)

GAGCCGCCCGCGTGGAGGGCTGCGAGCGCGCGCAAGGAACGGCAAGCGGGGCTGTGCCGCCCGACGACCGCC  
E P P A V E G C E P P R K E R Q G G L L P P D D R H

ACGACAGCGGGCTGGAATCCATGAAGGAGGAGGAGTACAGGCAGCTGGTGGGGGAGCTGGAGGACATCCGCCCTGCA  
D S G L D S M K E E Y R Q L V R E L E D I R L Q

GCCCCGAGCGCGCGCGCGCACGCCCTGGCGCCAGCAGCTACCGAGGACGGCGACACTTTTCTCCACTTG  
P R E P P A R P H A W A Q Q L T E D G D T F L H L

GCGATCATTCAGGAGGAAAGGCCCTGAGCCTGGAGGTGATCCGGCAGCGCGCTGGGACGCGCCTTCTGAACT  
A I I H E E K A L S L E V I R Q A A G D A A F L N F

Ank. I  
TCCAGAACAACCTCAGCCAGACTCCGCTCCACCTGGCGGTGATCACGGACCGCGGAAATCGCCGAGCACCTGCT  
Q N N L S Q T P L H L A V I T D Q A E I A E H L L

Ank. II  
GAAGGCTGGCTGCGACCTGGATGTGAGGACTTCCGTGGGAACACCCCGCTCCACATCGCCTGCCAGCAGGGCTCG  
K A G C D L D V R D F R G N T P L H I A C Q Q G S

Ank. III  
CTCCGACGCTCAGTGTCTCAGCAGCACTGCCAGCCCCACCACTCCTCGCCGTCTGAGGCCCACTACA  
L R S V S V L T Q H C Q P H H L L A V L Q A T N Y N

ACGGCCATACATGTCTCCATTGGCATCTATTCAAGGATACCTGGCTGTTGTGGAATACCTGCTGCTTAGGAGC  
G H T C L H L A S I Q G Y L A V V E Y L L S L G A

Ank. IV  
AGATGTAAATGCTCAGGAGCCATGCAATGGGAGAACAGCACTACACTTGGCCGTAGACCTTCAGAACTCAGACCTG  
D V N A Q E P C N G R T A L H L A V D L Q N S D L

Ank. V

Figure 43 (continued)

GTGTCACTTCTGGTGAAACACGGGCCAGATGTGAACAAAGTGACCTACCAGGGCTACTCCCCATACCAGCTTACAT  
V S L L V K H G P D V N K V T Y Q G Y S P Y Q L T W

GGGCAGAGACAACGCCAGCATACAGGAGCAGCTGAAGCTGCTGACCACAGCTGACCTGCAGATACTGCCCGAAAGT  
A E T T P A Y R S S 354

GAGGATGAGGAGAGCAGTGAATCAGAGCCAGAGTTCACAGAGGATGAACCTTATGTATGATGACTGCTGTATTGGAG  
GAAGACAGCTGACATTTTAAAGCAGAGGTTTCTGTGAGAAAGTGACTGTGTACATAATGTATAGGAAAAAAGCCTGA  
CTTTCCTTCATTTAAAAAGAAAGTCTATCTCGAAGGAGAAAAAAGTACTGAGATACTACACTGCCCAGCCAGGAGC  
ACATCATGCTAACAGGTTCCATGCTCTGACCTGTACTTAAGTAACGGGATGGGATGTGTAACATCGTTAAGAGATC  
AGTGAACATGCACACCATCTGATAAAGAGCCACGTTATCTAATTTCTCTGCCACATGAGGATAACGGACTGCACGT  
CCAATGTGCTGTTGTCAGAAATGCGTTTGAGAGCTGCCCTTGAGACACTAAGTCTGTGAGGAGTGCTCATCCCCCT  
CGGTGGCAAGACAGGCTTGACAAACGTCCTCATCTGCTTGAAGACTGTGAGGTTGGCATTAGGTTGAGGCACCTGCT  
GTGCCCCTGCTCCCTGACCCCTGGCTGCTCAGGGTTGAGGAGTCCGACCATGGGAGAGGTGACCTGGCTGCTGGGAGG  
AAGGTAGCAATGATGTAACTGTGGGCATTTGGAAACTGTGTGTTTACACACCATGTGTGTCTATAAATTGCTACACTT  
TTTAGCAACTGTATAGAATGTAAATACTGTACATCTTTGTTTATAATTATTTTGGTACCTGTGAGATATGTATTTA  
TTAAAAAAGGCAGATTTCTGTAAAAAA